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Dietary fiber intervention on gut microbiota composition in healthy adults: a systematic review and meta-analysis

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Short running head

Dietary fiber interventions on the gut microbiota

Abbreviations

CI – Confidence intervals

FISH – Fluorescence *in situ* hybridization

GI – Gastrointestinal

HMO – Human Milk Oligosaccharide

ICTRP – International Clinical Trials Register

MD – Mean difference

OTU – Operational taxonomic unit

PRISMA – Preferred Reporting Items for Systematic Reviews and Meta-Analysis

PROSPERO – The International Prospective Register of Systematic Reviews

qPCR – Quantitative polymerase chain reaction

RCT – Randomized controlled trial

SCFA – Short chain fatty acid

SD – Standard deviation

SE – Standard error

SMD – Standardized mean difference

Clinical trial registry number

Not required. PROSPERO registration (CRD42016053101)

URL: http://www.crd.york.ac.uk/PROSPERO/display_record.asp?ID=CRD42016053101

1 ABSTRACT

2 **Background:** Dysfunction of the gut microbiota is frequently reported as a manifestation of
3 chronic disease, and therefore presents as a modifiable risk factor in their development. Diet is
4 a major regulator of the gut microbiota and certain types of dietary fiber may modify bacterial
5 numbers and metabolism, including short-chain fatty acid (SCFA) generation.

6 **Objective:** A systematic review and meta-analysis were undertaken to assess the effect of
7 dietary fiber interventions on gut microbiota composition in healthy adults.

8 **Design:** A systematic search was conducted across MEDLINE, EMBASE, CENTRAL and
9 CINAHL for randomized controlled trials using culture and/or molecular microbiological
10 techniques evaluating the effect of fiber intervention on gut microbiota composition in healthy
11 adults. Meta-analyses using random-effects model were performed on alpha diversity, pre-
12 specified bacterial abundances including *Bifidobacterium* and *Lactobacillus* spp., and fecal
13 SCFA concentrations comparing dietary fiber intervention with placebo/low fiber
14 comparators.

15 **Results:** A total of 64 studies involving 2099 participants were included. Dietary fiber
16 intervention resulted in higher abundance of *Bifidobacterium* spp. [Standardized Mean
17 Difference (SMD) 0.64 (95% Confidence Interval: 0.42, 0.86]; $P < 0.00001$] and *Lactobacillus*
18 spp. [SMD: 0.22 (0.03, 0.41), $P = 0.02$] as well as fecal butyrate concentration [SMD: 0.24
19 (0.00, 0.47), $P = 0.05$] compared with placebo/low fiber comparators. Subgroup analysis
20 revealed fructans and galacto-oligosaccharides led to significantly greater abundance of both
21 *Bifidobacterium* spp. and *Lactobacillus* spp. compared with comparators ($P < 0.00001$ and $P =$
22 0.002 respectively). No differences in effect were found between fiber intervention and
23 comparators for α -diversity, abundances of other pre-specified bacteria, or other SCFA
24 concentrations.

25 **Conclusion:** Dietary fiber intervention, particularly involving prebiotic fibers, leads to higher
26 fecal abundance of *Bifidobacterium* and *Lactobacillus* spp. but does not impact α -diversity.
27 Further research is required to better understand the role of individual fiber types on the
28 growth of microbes and the overall gut microbial community.

29 **KEYWORDS**

30 Diet, dietary fiber, gastrointestinal microbiome, gastrointestinal microbiota, gut microbiota,
31 prebiotic

BACKGROUND

The gut microbiota is a highly diverse and metabolically active community, consisting of approximately 3.9×10^{13} microbial cells (1). These microbes participate in several functions beneficial to the host, including the fermentation of undigested nutrients (2, 3), synthesis of vitamins (4) and interaction with the immune system (5, 6). A number of disorders, including irritable bowel syndrome and type 2 diabetes mellitus, have been linked with disturbances in gut microbiota composition (2, 7-9). Such an association presents the gut microbiota as a potentially modifiable risk factor in the etiology of these conditions.

The gut microbiota can be detected and enumerated using different methods ranging from culture to next-generation sequencing (6, 10, 11), and can be characterized by measures of diversity and bacterial abundances (12, 13). Alpha diversity of the gut microbiota describes the richness (number of taxonomically distinct organisms present) and evenness (relative abundances of organisms) of its composition (12, 13), with cross-sectional studies demonstrating inverse associations between α -diversity and disease states (7-9). Specific bacteria shown to be more abundant in health compared with disease states include *Bifidobacterium* and *Lactobacillus* spp. (2, 7, 14), whose functions include carbohydrate fermentation and vitamin synthesis (15-18). Furthermore, increasing evidence supports the importance of 'keystone' bacterial species, whose absence may have profound consequences for the host, as well as other members of the microbial community and their metabolic outputs, including the short-chain fatty acid (SCFA) butyrate (19-23). Butyrate is of particular interest to health due to its beneficial properties such as its immunomodulatory effects (24, 25).

Dietary fiber is defined as non-digestible carbohydrates of ≥ 3 monomeric units found inherently in foods, and also includes isolated or synthetic fibers with demonstrated physiological benefits (26-28). It is a key candidate in facilitating changes in the gut microbiota, as it escapes digestion by the host in the small intestine to pass into the colon

where it is available to the microbial community. Dietary fiber encompasses an array of heterogeneous compounds whose physicochemical properties vary based on their particle size, chemical structure, solubility, viscosity and fermentability (29, 30). Fiber with fermentable characteristics are substrates for the microbial population in the colon, stimulating growth of specific organisms and leading to production of various metabolites including SCFA (19, 29, 31). Indeed, some fibers can be further classified as ‘prebiotic’ (e.g. fructans) if they have been shown to be selectively utilized by host microorganisms conferring a health benefit (32). The current body of evidence regarding the effect of dietary fiber on the gut microbiota is informed via specific prebiotic fiber interventions (33, 34), whole-diet interventions (35-37) and cross-sectional associations (38, 39). However, these investigations are limited in that prebiotic fibers represent only a subset of total dietary fiber, and confounding factors such as disease states and intake of other fermentable substrates, are unaccounted for in whole diet studies and cross-sectional studies (40). Therefore, there is a gap in knowledge regarding the precise impact of dietary fiber intervention on the gut microbiota in healthy subjects, and this is the focus on the systematic review.

METHODS

This systematic review was conducted in line with the guidelines of the Preferred Reporting Items for Systematic Reviews and Meta-Analysis: The PRISMA statement (41), and the guidelines of the Cochrane Handbook for Systematic Reviews and Interventions (42). The methods including the eligibility criteria, search strategy, extraction process and analysis were pre-specified and documented in a protocol that was published in the International Prospective Register of Systematic Reviews (CRD42016053101).

Literature search

A literature search was performed in the electronic databases MEDLINE, EMBASE, CENTRAL and CINAHL (from inception to October 4, 2017), using a combination of subject

headings, free text terms and synonyms relevant to this review, in consultation with an experienced systematic review search librarian (**Supplemental Tables 1-4**). There was no date or language restriction in the search strategy. A multi-step search approach was taken to retrieve relevant studies through additional hand-searching; contacting field experts; searching conference abstracts; theses and dissertations (ProQuest); and the International Clinical Trials Register (ICTRP) Search Portal and ClinicalTrials.gov to identify ongoing trials. Two review authors (DS and HS) screened articles in a blinded, standardized manner, with disagreements in judgement resolved by consensus or a third reviewer (KC).

Study selection

Search results were merged into reference management software Endnote (X7; Thomson Reuters) and de-duplicated prior to screening using Rayyan (Qatar Computing Research Institute) (43). Full text articles of potentially relevant studies were sought and reviewed. Attempts were made to contact the corresponding author where the full text article provided inadequate information to assess eligibility or extract relevant data. Studies were included if they met all of the following criteria: 1) randomized controlled trial (RCT), cluster RCT, or quasi-RCT; 2) inclusion of healthy adult participants (≥ 18 years of age); 3) intervention aimed at increasing fiber intake; 4) inclusion of a placebo for supplement interventions (e.g. maltodextrin), and either low fiber control (e.g. white bread) or habitual diet group for food interventions as comparators; 5) measured fecal microbiota related outcomes at the end of intervention.

Studies that were solely investigating enteral nutrition and those that included participants with an acute or chronic disease, including gastrointestinal (GI) conditions such as coeliac disease, inflammatory bowel disease, irritable bowel syndrome and other functional gastrointestinal disorders were excluded. Studies including mixed population groups where the healthy subgroup was not reported separately were also excluded. Studies that included overweight and

obese participants who were otherwise healthy and without any abnormal clinical parameters (e.g. elevated blood pressure) were included. Interventions eligible for inclusion provided an increase in fiber intake achieved through 1) dietary counselling to increase dietary fiber intake from food 2) food intervention (e.g. added cereals); or 3) fiber supplementation. Dietary counselling studies or food interventions were only included if fiber modification was the primary aim of the intervention.

The primary outcome was between-group differences in α -diversity of fecal microbiota at the end of the intervention. Measures of α -diversity included the total number of observed operational taxonomic units (OTUs) (the number of taxonomically-related groups of bacteria, evaluating richness); Chao1 Index (a non-parametric richness estimator); Shannon diversity index (a metric combining richness and evenness, with equal weighting to abundant and rare species); and Simpson diversity index (metric of richness and evenness, where more weighting is given to abundant species). Secondary outcomes were between-group differences in abundances of the following commonly measured bacterial groups: *Bifidobacterium* spp.; *Lactobacillus* spp.; *Roseburia* spp.; *Akkermansia muciniphila*; *Eubacterium hallii*; *Eubacterium rectale*; *Faecalibacterium prausnitzii*; and *Ruminococcus bromii*. Studies were included if they reported on either primary or secondary outcomes. Between-group differences in fecal SCFAs (total SCFAs and butyrate) were included as an exploratory outcome.

Data extraction and management

Two reviewers (DS and HS) independently extracted the data from eligible studies. Data extracted included: study design (duration, location, details of ‘run-in’ and ‘wash-out’ periods); participant characteristics, intervention details (fiber type, fiber dose, intervention delivery, compliance, assessment and control of dietary intake); and other information including antibiotic or probiotic use.

For all pre-specified primary, secondary and exploratory outcome data, the mean, standard deviation (SD), standard error (SE) or 95% confidence intervals (CI) that were reported at end of intervention were extracted for analysis. Where studies used multiple intervention groups of different fiber doses, data for the highest intervention dose was extracted. Where studies used multiple intervention groups of different fibers at the same dose compared with a single control group, data was extracted from each intervention group and pooled together. A weighted average of the intervention groups and the study variance was then calculated (44). Risk of bias was independently assessed by two reviewers (DS and HS) using Cochrane methodology (45). The review assessed “other bias” regarding the control of dietary intake during the study. This included examining whether dietary advice (e.g. to maintain dietary intake or avoid probiotic food sources) was provided, whether dietary compliance and/or intake were measured and reported, and if adjustments in statistical analysis were made if differences in dietary intake were found.

Statistical analysis

The overall treatment effect of fiber on primary and secondary outcomes was calculated using the difference between the end of intervention values for the intervention and comparator groups. Data reported as median and interquartile range were converted to mean and SD as previously described (46). Variance was calculated from the SD and SE of end of intervention values, or from the confidence intervals (CI) where these values were not available (46). In crossover studies, the mean and SD, SE or CI of intervention and control periods were extracted and analyzed separately (47). Where end of intervention endpoint data was unable to be obtained, the results were described in text only.

Meta-analysis was performed where outcomes were reported in at least two studies using Revman (Version 5.3; Cochrane Collaboration). The mean difference (MD) was used to calculate effect sizes where outcome data were presented in the same units (Shannon diversity

index, total number of observed OTUs). Where outcome data were reported using different units, effect sizes were calculated using the standardized mean difference (SMD) (bacterial abundances, fecal SCFA concentration).

A random-effects model was used to produce a pooled estimate of the MD or SMD, and the fixed-effects model was used to check for robustness and potential outliers. Inconsistencies between studies were assessed using the I^2 statistic, where significant heterogeneity was defined as $I^2 \geq 50\%$.

Pre-defined subgroup analyses were undertaken for primary and secondary outcomes that were reported in at least two studies in each subgroup. Pre-defined subgroup analyses included intervention types (supplements and dietary interventions), fiber types (accepted and candidate prebiotic fibers defined by Roberfroid et al., and general fibers defined by the review) (34), dose-response (comparing difference in fiber intake between intervention and control group of $\leq 5\text{g/d}$, $5\text{-}10\text{g/d}$, and $>10\text{g/d}$), trial design (parallel and crossover), and microbial analysis method (e.g. culture, sequencing). Post hoc subgroup analyses were undertaken for exploratory outcomes based on reporting method of fecal SCFA concentrations (dry weight of feces and wet weight of feces). Fructans and galacto-oligosaccharides were classified as ‘accepted prebiotic’ fibers, while ‘candidate prebiotic’ fibers included a broader range of fibers including polydextrose and resistant starch (34). The term ‘general fiber’ was used by the review to describe fibers not classified as either accepted or candidate prebiotics, and is not a formal term used to describe fibers in the literature.

For the fiber type subgroup analysis only, the fiber arm with the highest prebiotic classification (e.g. accepted prebiotic as opposed to a general fiber) was selected if multiple intervention groups were reported. Where multiple arms of the same prebiotic classification were presented, the interventions were pooled together and a weighted average of the intervention arms and study variance were calculated (44). Significant outliers were determined by visual

inspection as well as through a study-by-study sensitivity analysis, where each study was sequentially omitted and the remaining data re-assessed. If a study contributed to over 30% heterogeneity (based on changes to the I^2 statistic) then it was removed from the analysis in the sensitivity analysis. Funnel plots were generated for outcomes where at least 10 studies were included in meta-analysis (48) and reporting bias detected by assessment of funnel plot asymmetry by visual inspection.

RESULTS

Study characteristics

Study identification and selection are detailed in the PRISMA flow chart (**Figure 1**). The initial electronic and manual search generated 3829 records. After review of full texts (**Supplemental Table 5**), 64 publications, along with three secondary studies (49-51) reporting additional outcomes from the primary publications, fulfilled the inclusion criteria and were included in the review.

The 64 included primary studies that analyzed a total of 2099 participants. Of these 64 studies, 29 were parallel RCTs (52-80) and 35 were crossover RCTs (81-115). Five crossover trials did not include a wash out period (84, 93, 95, 105, 108). The majority of studies (52 studies) used fiber supplementation, including: accepted prebiotic fiber (26 studies) (52, 54-58, 61, 62, 65, 67, 70, 74, 86, 90, 92, 95, 97, 100, 102, 103, 105, 107, 109-111, 115); candidate prebiotic fiber (18 studies) (53, 63, 64, 66, 68, 69, 73, 77, 81, 83, 84, 87, 88, 91, 99, 101, 112, 113); general fiber (seven studies) (59, 60, 72, 76, 80, 93, 94); and a fiber mix (108). The remaining 12 studies used food intervention by providing key food items (e.g. wholegrain cereal) to supplement the diet (71, 78, 82, 85, 89, 96, 98) or provided all food and fluid to participants (75, 79, 104, 106, 114). Intervention doses ranged from 1.2 g/d to 50 g/d, while treatment periods ranged from five days to three months, with a median length of three weeks.

Analysis techniques used to characterize fecal microbiota included: culture (15 studies) (52, 54-58, 65, 66, 69, 71, 73, 96, 98, 105, 114); fluorescence *in situ* hybridization (FISH) (20 studies) (53, 70, 74, 76, 82, 85, 89-92, 94, 99, 100, 103, 106, 108-110, 112, 113); quantitative polymerase chain reaction (qPCR) (11 studies) (60, 63, 68, 81, 86, 87, 95, 102, 104, 107, 111); and next-generation sequencing (including 454 pyrosequencing and Illumina sequencing) (12 studies) (59, 62, 64, 72, 75, 77-80, 97, 101, 115). A combination of techniques were used in six studies (49, 61, 67, 83, 84, 88, 93).

The outcomes of each meta-analysis are reported in **Table 1**. Results from subgroup analyses performed are included in **Supplemental Table 6**. Overall, outcome data from 56 studies were suitable for meta-analysis; results from the following studies were unable to be statistically pooled and are presented narratively under their respective sub-headings (59, 62, 69, 77-79, 83, 93, 95, 97, 101, 113, 115). The characteristics of included studies are presented in **Tables 2-3**.

Dietary fiber and gut microbiota diversity (α -diversity)

Alpha-diversity was measured in 13 studies involving 393 participants (49, 59, 64, 72, 75, 77, 79, 80, 83, 88, 93, 97, 101).

Ten studies reported α -diversity using Shannon diversity index. Of these, six reported the metric in a form suitable for inclusion in the meta-analysis (49, 64, 72, 75, 80, 88). Dietary fiber intervention had no effect on α -diversity compared with placebo/low fiber comparators [MD: -0.06 Shannon diversity index (95% CI: -0.25, 0.12), $P = 0.48$], albeit with substantial heterogeneity ($I^2 = 53\%$). In two of the studies not included in the meta-analysis, raffinose and resistant starch interventions did not lead to significant difference in α -diversity compared with placebo (93, 101). A significant reduction in the α -diversity of fecal microbiota from baseline was detected in a trial involving flaxseed mucilage, measured by both the exponential of Shannon diversity index [-38010 (95% CI: -64473, -11546, $P = 0.007$)] as well as through

Simpson's inverse index [-17515 (95% CI: -30992, -4038, $P = 0.014$)], although a between-group comparison was not reported (59). Conversely, significant end of intervention differences in α -diversity measured by Shannon diversity index ($P = 0.013$) and inverse Simpson index ($P = 0.004$) were detected between intervention and comparator groups in a supplementation trial involving resistant starch type 2 (77).

A study evaluating α -diversity through Simpson's index found it was significantly higher in the intervention group receiving polydextrose compared with placebo after 21 days ($P = 0.014$) (88). A trial involving 15 g/d arabinoxylan supplementation reported variable intervention effects when α -diversity was evaluated using different metrics: α -diversity was significantly lower compared with placebo when measured through observed species ($P = 0.029$), but there were no significant differences when assessed by Simpson's evenness ($P = 0.063$) (80).

A separate meta-analysis was performed for the three studies reporting α -diversity measured by total number of observed OTUs (49, 72, 75). Dietary fiber had no effect on α -diversity compared with placebo/low fiber comparators [MD: -4.37 OTUs (95% CI: -42.92, 34.19), $P = 0.82$], with no heterogeneity ($I^2 = 0\%$). The Chao1 index was used to report α -diversity in two studies, although there was insufficient data available precluding meta-analysis. Neither trial reported significant differences between fiber intervention and placebo or low fiber control (49, 83). A feeding trial comparing wholegrain and refined grain diets found no difference in α -diversity at end of intervention between the two groups, although the metric used to measure α -diversity was not reported (79).

Dietary fiber and bacterial abundances

Reporting of bacterial abundances differed across studies. Of the taxa of interest in this review, abundances of *Bifidobacterium* spp. (59 studies) and *Lactobacillus* spp. (28 studies) were most commonly reported. No studies reported on the abundance of *Akkermansia muciniphila*.

A total of 59 studies including 1896 participants reported the effect of dietary fiber on *Bifidobacterium* spp. abundance and of these, 51 trials (1629 participants) reported data in a form suitable for meta-analysis (53-58, 60, 61, 63-68, 70, 71, 73-76, 81, 82, 84-94, 96-112, 114). Dietary fiber led to a significantly greater *Bifidobacterium* spp. abundance compared with placebo/low fiber comparators [SMD: 0.64 (95% CI: 0.42, 0.86), $P < 0.00001$], albeit with considerable heterogeneity ($I^2 = 85\%$) (**Figure 2**).

However, subgroup analysis showed fiber interventions delivered through supplements resulted in a significantly higher *Bifidobacterium* spp. abundance compared with placebo/low fiber controls [SMD: 0.75 (95% CI: 0.52, 0.98), $P < 0.00001$, $I^2 = 83\%$], whereas no differences were found between food interventions and comparators [SMD: 0.20 (95% CI: -0.36, 0.76), $P = 0.49$, $I^2 = 88\%$], although considerable heterogeneity persisted in both analyses.

Subgroup analysis demonstrated interventions investigating fibers classified as accepted prebiotics and candidate prebiotics resulted in a significantly higher *Bifidobacterium* spp. abundance compared with placebo/low fiber controls [Accepted prebiotic fiber SMD: 0.68 (95% CI: 0.38, 0.98), $P < 0.00001$, $I^2 = 81\%$; Candidate prebiotic fiber SMD: 0.77 (95% CI: 0.30, 1.24), $P < 0.00001$, $I^2 = 86\%$] (**Figure 2**). However, there was no difference in effect between the general fiber subgroup compared with comparators [SMD: 0.25 (95% CI: -0.16, 0.65), $P = 0.24$, $I^2 = 86\%$]. This subgroup analysis did not reduce the considerable heterogeneity across each subgroup.

Subgroup analysis of dose-response showed dietary fiber led to significantly higher *Bifidobacterium* spp. abundance compared with placebo/low fiber comparators at all pre-defined dosage [≤ 5 g/d fiber SMD: 0.51 (95% CI: 0.18, 0.84), $P = 0.003$, $I^2 = 70\%$; 5-10g/d SMD: 0.48 (95% CI: 0.13, 0.83), $P = 0.007$, $I^2 = 87\%$; >10 g/d SMD: 0.85 (95% CI: 0.45, 1.25),

279 $P < 0.00001$, $I^2 = 85\%$]. No differences were found in subgroup analyses of trial design or
 280 microbiota analysis method (**Supplemental Table 6**).
 281 Eight trials were not included in the meta-analysis. In the supplement trials of accepted
 282 prebiotics, a significantly higher *Bifidobacterium* spp. abundance was reported following
 283 supplementation involving inulin (115) and human milk oligosaccharides (HMO) (62)
 284 compared with placebo at the end of intervention, while a significant within-group increase
 285 from baseline was detected following 10g/d inulin supplementation (95). In the candidate
 286 prebiotic trial of resistant starch supplementation, *Bifidobacterium* spp. abundance was
 287 significantly higher in the intervention group compared with placebo at end of intervention
 288 (77). In the supplement studies of general fiber, *Bifidobacterium* spp. abundance was higher
 289 following after xylo-oligosaccharide supplementation compared with placebo (69) while
 290 manno-oligosaccharides had no effect on *Bifidobacterium* spp. compared with placebo (113).
 291 The third supplement trial of general fiber (resistant maltodextrin) reported no change in
 292 *Bifidobacterium* spp. abundance within groups using FISH, although a significant increase
 293 from baseline was reported for the intervention group on qPCR analysis (83). Finally, a food
 294 study comparing intakes of wholegrains to refined grain products found no significant
 295 difference in *Bifidobacterium* spp. abundance at the end of intervention period (78).
 296 *Lactobacillus* spp. abundance was measured in 28 studies involving 867 participants. Data
 297 from 24 studies (730 participants) was reported in a form suitable for meta-analysis (52, 55,
 298 56, 60, 63-68, 73, 75, 76, 84, 87, 93, 96, 97, 99, 104, 105, 107, 111, 114). Dietary fiber led to a
 299 significantly greater *Lactobacillus* spp. abundance compared with placebo/low fiber
 300 comparators [SMD: 0.37 (95% CI: 0.07, 0.68), $P = 0.02$]. However, heterogeneity was
 301 considerable ($I^2 = 80\%$), and was skewed by results from a single outlier study (66) [4.70 (95%
 302 CI: 3.69, 5.70)]. A sensitivity analysis excluding this study produced a more homogenous
 303 study population ($I^2 = 49\%$), with a modest impact on the result [SMD: 0.22 (95% CI: 0.03,

0.41), $P = 0.02$] (**Figure 3**). The outlier study (66) was excluded from subsequent subgroup analyses.

Subgroup analysis demonstrated interventions involving fiber supplements resulted in a significantly higher *Lactobacillus* spp. abundance compared with placebo/low fiber controls while substantially reducing study heterogeneity [SMD: 0.16 (95% CI: 0.01, 0.31), $P = 0.04$, $I^2 = 7\%$]. No significant differences in effect were found between food interventions and comparators [SMD: 0.35 (95% CI: -0.46, 1.16), $P = 0.40$, $I^2 = 84\%$].

Subgroup analysis of fiber types showed accepted prebiotic fiber interventions led to a significantly greater *Lactobacillus* spp. abundance compared with placebo/low fiber controls and further reduced heterogeneity [SMD: 0.34 (95% CI: 0.13, 0.55), $P = 0.002$, $I^2 = 0\%$] (**Figure 3**). There were no differences in effect in the candidate prebiotic [SMD: -0.06 (95% CI: -0.29, 0.16), $P = 0.58$, $I^2 = 0\%$] and general fiber [SMD: 0.22 (95% CI: -0.31, 0.75), $P = 0.42$, $I^2 = 74\%$] subgroups when compared with comparators.

Subgroup analysis of analysis method demonstrated dietary fiber led to significantly higher *Lactobacillus* spp. abundance compared with placebo/low fiber comparators when enumerated via culture [SMD: 0.61 (95% CI: 0.13, 1.08), $P = 0.01$]. There were no significant differences between intervention and comparator when *Lactobacillus* spp. was detected using FISH, qPCR or sequencing (**Supplemental Table 6**). There were no differences in effect when sub-analyzing by intervention type or dose-response (**Supplemental Table 6**).

There were four studies that could not be pooled into the meta-analysis. A prebiotic supplementation trial of HMOs reported no difference in *Lactobacillus* spp. abundance between intervention and control groups (62). There was also no significant difference in *Lactobacillus* spp. reported in a wholegrain food intervention study compared with controls (78). Of the two remaining studies, there was higher *Lactobacillus* spp. abundance following xylo-oligosaccharide supplementation compared with placebo (69), and significant within-

group increases in *Lactobacillus* spp. abundance was demonstrated following manno-oligosaccharide supplementation (113).

Abundance of *F. prausnitzii* was measured in 15 studies investigating 566 participants. Thirteen studies (519 participants) were able to be meta-analyzed (53, 61, 67, 68, 74, 84, 88, 94, 99-101, 110, 112). There was no difference between dietary fiber compared with placebo/low fiber comparators for *F. prausnitzii* abundance [SMD: 0.14 (95% CI: -0.12, 0.39), $P = 0.29$], with substantial heterogeneity between studies ($I^2 = 68\%$) (**Figure 4**). Aside from trial design, no differences with respect to the pre-specified subgroups were found (**Supplemental Table 6**). Two studies reporting abundances of *F. prausnitzii* were unable to be pooled into the meta-analysis. Both studies measured the relative abundance of *F. prausnitzii* and reported only within-group changes, with one study reporting a decrease in abundance following supplementation of flaxseed mucilage (59), and the other reporting an increase in abundance following inulin supplementation (50).

Seven studies including 261 participants measured *Roseburia* spp. abundance. Four studies (189 participants) were included in the meta-analysis (49, 68, 79, 97). Dietary fiber had no effect on *Roseburia* spp. abundance compared with placebo/low fiber comparators [SMD: 0.33 (95% CI: -0.14, 0.80), $P = 0.17$] although substantial heterogeneity was detected ($I^2 = 70\%$) (**Figure 4**). Similar results were reported in the studies excluded from meta-analysis. No between or within-group differences were detected between intervention and placebo groups in two prebiotic fiber supplement trials (50, 62). A third trial found the relative abundance of *Roseburia* spp. was lower following inulin supplementation compared with control at end of intervention, although significance was not reported (115).

Two studies of 32 participants measured *E. hallii* abundance. These results could not be statistically pooled because one study did not report data in a suitable form. One study

reported no within-group difference in *E. hallii* abundance (50, 62), the other reported a significant decrease in *E. hallii* abundance compared with placebo (49). *E. rectale* was measured in three studies including 42 participants. Two studies (30 participants) were suitable for meta-analysis (84, 101). Dietary fiber did not impact on *E. rectale* abundance compared with placebo/low fiber comparators [SMD: -0.26 (95% CI: -1.20, 0.67), $P = 0.58$] and substantial heterogeneity was detected ($I^2 = 75\%$) (**Figure 4**). The study not eligible for meta-analysis was an inulin supplementation trial which reported no difference for within-group effects for *E. rectale* abundance (50). *R. bromii* abundance was measured in three studies encompassing 76 participants, of which all were suitable for meta-analysis (49, 81, 101). Dietary fiber had no effect on *R. bromii* abundance compared with placebo/low fiber comparators [SMD: 0.15 (95% CI: -0.15, 0.45), $P = 0.33$], with no heterogeneity detected ($I^2 = 0\%$) (**Figure 4**).

Dietary fiber and short-chain fatty acids

A total of 25 studies of 870 participants reported between-group differences in fecal SCFA concentration following fiber intervention (52, 53, 55, 59, 63, 64, 66-68, 71, 73, 74, 77, 80, 82, 84, 86, 90, 91, 93, 94, 96, 103, 112, 115). Fecal SCFA concentration was determined through gas-liquid chromatography in all but one study (90) where high-performance liquid chromatography was used.

Total fecal SCFA concentration was measured in 13 studies encompassing 406 participants (52, 55, 59, 63, 64, 67, 73, 80, 82, 84, 86, 91, 94). Dietary fiber had no effect on total SCFA concentration compared with placebo/low fiber comparators [SMD: 0.11 (95% CI: -0.05, 0.27), $P = 0.19$], with similar intervention effects across studies ($I^2 = 0\%$).

Fecal acetate concentration was reported in 18 studies involving 657 participants (52, 53, 63, 66, 71, 74, 77, 80, 82, 84, 86, 90, 91, 93, 94, 96, 103, 112). There was no difference in fecal

377 acetate following fiber intervention compared with placebo/low fiber comparators [SMD: 0.28
 378 (95% CI: -0.08, 0.63), $P = 0.13$] with substantial heterogeneity between studies ($I^2 = 86$).
 379 The effect of fiber intervention on fecal propionate concentration was reported in 19 studies of
 380 677 participants (52, 53, 63, 66, 71, 74, 77, 80, 82, 84, 86, 90, 91, 93, 94, 96, 103, 112, 115).
 381 No differences were found between fecal propionate and comparators [SMD: -0.01 (95% CI: -
 382 0.20, 0.22), $P = 0.95$], with moderate heterogeneity detected ($I^2 = 61\%$).
 383 The effect of fiber intervention on fecal butyrate concentration was reported in 20 studies of
 384 712 participants (52, 53, 59, 63, 66, 71, 74, 77, 80, 82, 84, 86, 90, 91, 93, 94, 96, 103, 112,
 385 115). Fecal butyrate was significantly higher following fiber intervention compared with
 386 placebo/low fiber comparators [SMD: 0.24 (95% CI: 0.00, 0.47), $P = 0.05$], although
 387 considerable heterogeneity was present ($I^2 = 70\%$).
 388 Of the studies evaluating differences in fecal SCFA concentration following fiber intervention
 389 compared with placebo/low fiber comparators, 13 studies expressed mean SCFA
 390 concentrations per wet weight of feces (52, 53, 66, 67, 71, 73, 74, 77, 82, 90, 91, 96, 115), 10
 391 studies as dry weight of feces (55, 59, 63, 64, 68, 80, 93, 94, 103, 112), one study as molar
 392 ratio (84), and one study as a combination of wet weight of feces and molar ratio (86).
 393 Additional subgroup analyses were performed to compare differences in fecal SCFA
 394 concentrations when expressed as wet weight compared with dry weight (**Supplemental**
 395 **Table 7**). Fiber intervention led to significantly higher fecal concentrations of total SCFA,
 396 acetate and butyrate compared with comparators when expressed per wet weight of feces.
 397 However, there were no significant differences when mean SCFA concentrations were
 398 expressed per dry weight of feces. Study heterogeneity was considerably greater for fecal
 399 acetate and butyrate, but not total fecal SCFA concentrations when expressed as wet compared
 400 with dry wet of feces. There were no differences in effect based on analysis method for fecal

propionate concentrations, although heterogeneity was greater when results were expressed per wet weight of feces (**Supplemental Table 7**).

Differences in intervention effects based on trial design

There were differences in intervention effects in subgroup analyses depending upon trial design. Dietary fiber led to significantly lower α -diversity compared with placebo/low fiber comparators in crossover design trials, where α -diversity was reported using Shannon diversity index [MD: -0.10 (95% CI: -0.19, -0.01), $P = 0.03$], while there was no difference in α -diversity in parallel design trials [MD: -0.03 (95% CI: -0.57, 0.51), $P = 0.91$] (**Supplemental Table 6**). The presence and duration of washout periods were inconsistent across the three crossover trials included this analysis. One study did not include a wash out period (84), and wash out periods lasted 14 (75) and 21 days (88) in the other two. Regarding bacterial abundances however, intervention effects were significant in parallel trials but not in crossover trials for *Lactobacillus* and *Roseburia* spp. and *F. prausnitzii*, but not for *Bifidobacterium* spp. (**Supplemental Table 6**). Statistical heterogeneity was lower in crossover trials compared with parallel trials for α -diversity reported using Shannon diversity index, *Bifidobacterium* and *Lactobacillus* spp., as well as *F. prausnitzii*, but there was no difference in statistical heterogeneity for *Roseburia* spp. (**Supplemental Table 6**).

Risk of bias

The risk of bias was low-to-moderate across the 64 included studies (**Supplemental Figure 1**). Selection bias was unclear in most studies. Random sequence generation and allocation concealment were adequately described by 26% (59-62, 70-72, 77, 79, 80, 84, 86, 94, 103, 113-115) and 16% (59, 61, 62, 70, 77, 79, 80, 86, 94, 115) of studies, respectively. There was low risk of bias across included studies regarding performance and detection bias, as most trials investigated objective outcomes and incorporated a double-blind design. Attrition bias was adequately addressed by only 41% (54-58, 62, 67, 69, 71, 74-76, 79, 82, 86-89, 92, 93, 98,

99, 105, 107, 108, 110) of the included studies. Selective reporting was unclear in the majority of studies. Published protocols or clinical registrations were reported by only 26% (59, 61, 68-70, 75, 77-80, 86, 97, 100-102, 110, 115) of included studies. Bias related to control of dietary intake was unclear in half of included studies (55%) (54, 56-60, 62, 64-67, 71, 72, 74, 78, 80, 81, 83, 85-93, 96, 98, 102, 103, 105, 108, 110, 115), while even fewer studies were judged to have a low risk of bias regarding dietary advice and assessment of dietary compliance (33%) (52, 55, 63, 68, 69, 73, 75, 76, 79, 82, 84, 94, 97, 99, 104, 106, 107, 111-114). Furthermore, 13% (53, 61, 70, 77, 95, 100, 101, 109) of studies did not provide dietary advice or assess intake, and were judged to have a high risk of bias relating to the potential influence of background dietary intake.

Reporting bias

Funnel plots were generated for abundances of *Bifidobacterium* spp.; *Lactobacillus* spp.; *F. prausnitzii*; and total SCFA; acetate; propionate; and butyrate concentrations. Visual inspection found no evidence of funnel plot asymmetry, indicating reporting bias was unlikely (Supplemental Figures 2-7).

DISCUSSION

This systematic review and meta-analysis found dietary fiber intervention had no effect on the diversity of the gut microbiota but did increase abundance of *Bifidobacterium* and *Lactobacillus* spp. as well as fecal butyrate concentration in healthy adults.

The lack of effect on α -diversity of the gut microbiota found in this review is similar to other dietary interventions documented in the literature. For instance, controlled feeding studies lasting four days to three weeks found that despite significant changes to fiber intake, there was no effect on microbial diversity (35-37). These findings suggest that short-term dietary interventions are unlikely to facilitate changes in the α -diversity of the gut microbiota. Indeed, study design is likely important, as subgroup analysis demonstrated different effects between crossover and parallel trials. The lower α -diversity between fiber and control groups in crossover trials may be related to a lack of or insufficient wash-out between interventions, as well as potential differences in the microbiota and habitual diet of individuals at baseline. These null findings are in contrast to the findings from observational studies that report a correlation between fiber intakes in habitual diet and diversity of the gut microbiota, for example in studies comparing agrarian dietary habits with Western populations (38, 39). Interestingly, a positive correlation has also been reported between dietary diversity and microbiota diversity (116). Taken together, long term dietary diversity as opposed to changes in isolated nutrients or foods over a short period of time may be a stronger driver of microbial diversity. It must also be noted that the stability of the gut microbiota, as well as the abundances and metabolites of the individual members of the microbial community, also contribute to maintaining an ecosystem that promotes health (117, 118). Therefore, the totality of findings here, including that microbial diversity was not compromised, support the favorable effects of dietary fiber on the gut microbiota.

In regard to particular bacterial groups, this review demonstrated dietary fiber interventions involving accepted prebiotic fibers led to higher abundance of *Bifidobacterium* and *Lactobacillus* species. These results support the selectivity criteria of the prebiotic concept, where the host microorganisms selectively utilize the prebiotic fibers as substrates, which may confer health benefits to the host (32). However, candidate prebiotic interventions produced different effects on the abundance of these two genera, with significant effects demonstrated for *Bifidobacterium* but not *Lactobacillus* species. This may represent differences in substrate preferences between the two genera, where *Bifidobacterium* spp. may be less discriminating than *Lactobacillus* spp. regarding fermentation substrates (119, 120). Conversely, fibers not classified as accepted or candidate prebiotics, here termed general fibers, did not impact the abundance of these taxa. This may be due to the heterogeneity of the general fibers, including their degree of polymerization, viscosity and fermentability, whereas accepted and candidate prebiotic fibers are mostly highly fermentable oligosaccharides (29, 30).

Subgroup analysis separating the effect of food vs supplement interventions showed food interventions had no effect on *Bifidobacterium* and *Lactobacillus* species. This result may be attributed to a lack of statistical power, due to the food interventions comprising a relatively small number of low sample size studies (10 studies, 301 participants; 4 studies, 127 participants). It must also be noted that most of the trials employing food interventions supplemented with grain and cereal foods to increase fiber intake (71, 78, 79, 82, 85, 89, 96, 98, 104). Therefore, the food interventions evaluated may be more representative of grains and cereals *per se* rather than a diverse range of fibrous foods.

Interestingly, there were no differences in the effect of dietary fiber interventions on *Bifidobacterium* spp. abundance with varying doses of fiber. Dietary fiber intervention led to an effect at all levels of consumption in subgroup analysis (≤ 5 g, 5-10g, >10 g) with no discernible gradient in effectiveness, suggesting fewer than 5 grams of dietary fiber is

sufficient. This may represent a potential limit to the amount of fiber that can be fermented by *Bifidobacterium* species. The lack of a dose-response effect may also be attributed to the percentage increase in fiber intake from baseline rather than the intervention dose, which was unable to be accounted for in this review due to the inconsistent reporting of baseline values across included studies. This requires further clarification but lower dose supplementation may be advantageous in patients who experience GI symptoms with higher fiber loads.

There was more variability in intervention effects for abundances of *Bifidobacterium* spp. ($I^2 = 85\%$) compared with *Lactobacillus* spp. ($I^2 = 49\%$). While this may be related to differences in the accuracy of techniques used to determine specific bacterial abundances (121, 122), there were no differences in effect based on analysis method for *Bifidobacterium* species. Another plausible explanation is the differences in nutrient requirements of these taxa as discussed previously. Furthermore, ‘responder and non-responder’ effects for *Bifidobacterium* spp. abundance, which have been shown previously (97, 123, 124), may be impacted by individual host factors, such as differences in baseline abundances (124), or the presence/absence of specific strains of *Bifidobacterium* able to utilize the particular fiber under investigation.

There were differences in intervention effects based on trial design, with parallel design studies demonstrating stronger intervention effects and greater statistical heterogeneity compared with crossover design studies for several outcomes. This may in part be due to inter-individual differences in microbiota composition as well as carry-over effects from a lack of or insufficient wash-out periods in the crossover studies as discussed previously.

There was no effect of dietary fiber interventions on abundance of other commonly measured bacterial groups (e.g. *F. prausnitzii*), suggesting these species may be stimulated by dietary components other than fiber, such as polyols and polyphenols (125). However, the number of studies evaluating species of other bacterial groups was small, and therefore further studies are needed to investigate the effect of fiber and other dietary components on these groups.

515 The higher fecal concentration of butyrate following fiber intervention highlights the ability of
516 dietary fiber to beneficially modulate the metabolic outputs of the gut microbiota. This is
517 likely due to cross-feeding interactions between butyrate producers with *Bifidobacterium* and
518 *Lactobacillus* species, which are noted lactate and acetate producers (25, 120, 126). As the
519 preferred energy source for colonic epithelial cells, butyrate is a microbial by-product that is of
520 particular interest to host health, exhibiting a wide spectrum of positive effects, such as
521 inhibiting colonic carcinogenesis and ameliorating mucosal inflammation (31, 127, 128).
522 However, it is acknowledged that the variability in the reporting of SCFA results may limit the
523 applicability of these findings, particularly when considering the variance in results when
524 expressed as wet compared with dry weight of feces.

525 This study is the first systematic review and meta-analysis to assess the effect of dietary fiber
526 intervention on gut microbiota composition. Major strengths of this study include its robust
527 design, comprehensive search strategies, and the use of two independent reviewers.

528 It is acknowledged this study has some limitations. Firstly, there were only a limited number
529 of studies reporting the primary outcome of α -diversity, and a small proportion presenting data
530 using the same diversity indices. Secondly, baseline fiber intake was not able to be accounted
531 for due to the paucity of reporting by included studies. Furthermore, included studies sampled
532 feces as a surrogate for gut microbiota profile, and although feces are a common sampling
533 route, the microbial composition of feces differs from the mucosal microbiota (10, 11), which
534 is in closer contact with the host and may be more important when considering the relationship
535 between microbiota and disease pathophysiology or outcomes. Finally, the limited number of
536 taxa assessed in the review may not convey the overall effect elicited by dietary fiber
537 intervention on gut microbiota composition and metabolic outputs, although the selection of
538 taxa was guided by the available literature. Thus, the taxa selected may be more representative
539 of the scope of research in the field to date, rather than a limitation of the review.

540 Dietary fiber intervention leads to a higher abundance of fecal *Bifidobacterium* and
541 *Lactobacillus* spp., as well as higher fecal concentration of butyrate compared with
542 placebo/low fiber comparators. Accepted prebiotic fibers had an effect on the abundances of
543 both *Bifidobacterium* and *Lactobacillus* spp. while candidate prebiotic fibers had an effect on
544 *Bifidobacterium* spp. abundance but not *Lactobacillus* species. General fibers appear to have a
545 limited effect on gut microbiota composition. Although the diversity of the gut microbiota,
546 abundances of other commonly measured bacterial groups and concentration of other fecal
547 SCFAs were not significantly different compared with controls following dietary fiber
548 intervention, it is worth noting that a short-term increase in fiber intake does not appear to be
549 rate-limiting to these outcomes. These results further support the favorable effects of dietary
550 fiber and contribute to our understanding of its effect on the gut microbiota.

551 Future RCTs investigating the effect of fiber on the gut microbiota should adjust for
552 participants' baseline microbiota composition and dietary characteristics as well as controlling
553 for dietary intake in order to determine the precise effect of dietary fiber. Scope may also need
554 to be broadened to evaluate taxa than that considered here, including the eukaryote (e.g. fungi)
555 members of the gut microbiota. Additionally, longer duration studies are needed to better
556 assess the chronic effect of fiber on microbiota diversity.

557 **Author contributions**

558 The author's responsibilities were as follows – HS and KC: initiated the study; DS, KW, HS,
559 MR, KW and KC: developed the protocol; DS and HS: performed eligibility screening and
560 data extraction; DS and JK: analyzed the data and performed the statistical analysis; DS KW,
561 MR, MM, JK, ES, HS and KC: interpreted the data; DS: wrote the initial manuscript; and KW,
562 MR, MM, GH, JK, ES, HS and KC: critically revised the manuscript. All authors read and
563 approved the final manuscript.

564 **Competing interests**

565 None declared.

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Table 1: Statistical analysis for the outcomes reported in ≥ 2 randomized controlled trials and included in the meta-analysis.

| Outcomes | No. of studies in meta-analysis (references) | n^I | Results | | Heterogeneity | | |
|--|---|-------|---|----------|-----------------|----------|-----------|
| | | | Meta-analysis overall estimate (95% CI) | P | Chi-square test | P | I^2 (%) |
| Shannon Diversity Index | 6 (64, 72, 75, 80, 84, 88) | 127 | MD: -0.06 (95% CI: -0.25; 0.12) | 0.48 | 10.73 | 0.06 | 53 |
| Total number of observed OTUs | 3 (72, 75, 84) | 53 | MD: -4.37 (95% CI: -42.92; 34.19) | 0.82 | 0.07 | 0.97 | 0 |
| <i>Bifidobacterium</i> spp. | 51 (52-58, 60, 61, 63-68, 70-76, 82, 84-94, 96-112, 114) | 1629 | SMD: 0.64 (95% CI: 0.42; 0.86) | <0.00001 | 327.93 | <0.00001 | 85 |
| <i>Lactobacillus</i> spp.² | 23 (52, 55, 56, 60, 63-65, 67, 68, 73, 75, 76, 84, 87, 93, 96, 97, 99, 104, 105, 107, 111, 114) | 670 | SMD: 0.22 (95% CI: 0.03; 0.41) | 0.02 | 42.8 | 0.005 | 49 |
| <i>Faecalibacterium prausnitzii</i> | 13 (53, 61, 67, 68, 74, 84, 88, 94, 99-101, 110, 112) | 519 | SMD: 0.14 (95% CI: -0.12; 0.39) | 0.29 | 37.53 | 0.0002 | 68 |
| <i>Roseburia</i> spp. | 4 (68, 79, 84, 97) | 189 | SMD: 0.33 (95% CI: -0.14; 0.80) | 0.17 | 10.16 | 0.02 | 70 |
| <i>Eubacterium rectale</i> | 2 (84, 101) | 30 | SMD: -0.26 (95% CI: -1.20; 0.67) | 0.58 | 3.94 | 0.05 | 75 |
| <i>Ruminococcus bromii</i> | 3 (81, 84, 101) | 76 | SMD: 0.15 (95% CI: -0.15; 0.45) | 0.33 | 1.1 | 0.58 | 0 |
| Total SCFA | 13 (52, 55, 59, 63, 64, 67, 73, 80, 82, 84, 86, 91, 94) | 406 | SMD: 0.11 (95% CI: -0.05; 0.27) | 0.19 | 6.46 | 0.89 | 0 |
| Acetate | 18 (52, 53, 63, 66, 71, 74, 77, 80, 82, 84, 86, 90, 91, 93, 94, 96, 103, 112) | 657 | SMD: 0.28 (95% CI: -0.08; 0.63) | 0.13 | 119.36 | <0.00001 | 86 |
| Propionate | 19 (52, 53, 63, 66, 71, | 677 | SMD: 0.01 (95% CI: -0.20; 0.22) | 0.95 | 46.23 | 0.0003 | 61 |

| Outcomes | No. of studies in meta-analysis (references) | <i>n</i> ¹ | Results | | Heterogeneity | | |
|-----------------|--|-----------------------|---|----------|-----------------|----------|--------------------|
| | | | Meta-analysis overall estimate (95% CI) | <i>P</i> | Chi-square test | <i>P</i> | I ² (%) |
| Butyrate | 74, 77, 80, 82, 84, 86, 90, 91, 93, 94, 96, 103, 112, 115) 20 (52, 53, 59, 63, 66, 71, 74, 77, 80, 82, 84, 86, 90, 91, 93, 94, 96, 103, 112, 115) | 712 | SMD: 0.24 (95% CI: 0.00; 0.47) | 0.05 | 64.21 | <0.00001 | 70 |

Data was meta-analyzed using a random-effects model and presented as MDs or SMDs as appropriate. Statistical heterogeneity was assessed using the chi-square test and quantified using the I² statistic. ¹ Number of participants in meta-analysis. ² Results from outlier study excluded from this meta-analysis. Abbreviations: MD, Mean difference; OTU, Operational taxonomic unit; SCFA, Short chain fatty acid; SMD, Standardized mean difference.

Table 2: Characteristics of randomized controlled trials of fiber supplementation comparing dietary fiber with placebo or low fiber comparators in healthy adults

| Study | Participants | | Interventions | | | RCT Design | | | | |
|---|--|--|---------------|-----------------------------|-------------------------|------------|-----------------|--------|----------|--------------------------------------|
| | n; age ¹ ; % F | Fiber, daily dose | Prebiotic | Comparator; daily dose | Compliance ² | Design | Duration (days) | Run in | Wash out | Analysis |
| Abell 2008 (81) | 46; 25-66; 65% | RS, 22 g | C | RS, 1 g | Y | Cross-over | 28 | Y | Y | qPCR |
| Alfa 2017 (77) | 84; 32-96; 42% | RS2, 21 g | C | Corn starch, 21 g | Y | Parallel | 72 | Y | N | Illumina |
| Alles 1999 (52) | 27.4; 40.4; 45% | TOS, 15 g | A | Glucose & lactose mix, 15 g | Y | Parallel | 21 | Y | N | Culture |
| Baer 2014 (83) | 14; 47; 9% | Resistant maltodextrin, 50 g | C | Maltodextrin, 50 g | Y | Cross-over | 21 | N | Y | 454 Pyrosequencing; DGGE; FISH; qPCR |
| Beards 2010 (53) | 30; 33 ³ ; 66% ³ | PDX; RS, 45.6 g | C | Maltitol, 45.6 g | N | Parallel | 44 | N | N | FISH |
| Blaedel 2016 (115) | 21; 23-45; 100% | Inulin, 15 g | A | Placebo | Y | Cross-over | 21 | N | Y | Illumina |
| Boler 2011 (84); Hooda 2012 (49)⁴ | 21; 21-28; 0% | PDX⁵ ; Soluble maize fiber, 21 g | C | Placebo | N | Cross-over | 21 | N | N | qPCR; Pyrosequencing ⁴ |
| Bouhnik 1996 (54) | 10; 22-39; 50% | SC-FOS, 12.5 g | A | Saccharose, 10 g | N | Parallel | 12 | Y | Y | Culture |
| Bouhnik 1999 (58) | 8; 29.6; 55% | SC-FOS, 20 g | A | Saccharose, 20 g | N | Parallel | 7 | N | N | Culture |

| Study | Participants | | Interventions | | | RCT Design | | | | |
|----------------------------|--|---|---------------|----------------------------------|-------------------------|------------|-----------------|--------|----------|--------------------------------|
| | n; age ¹ ; % F | Fiber, daily dose | Prebiotic | Comparator; daily dose | Compliance ² | Design | Duration (days) | Run in | Wash out | Analysis |
| Bouhnik 2004 (57) | 64; 30 ³ ; 55% ³ | SC-FOS ⁵ ; GOS ⁵ ; Isomaltos; Inulin ⁵ ; RS; Soybean-OS, 10 g | A | Sucrose & maltodextrin mix, 10 g | N | Parallel | 7 | Y | N | Culture |
| Bouhnik 2006 (56) | 40; 29; 55% | SC-FOS (Actilight), 10 g | A | Sucrose & maltodextrin mix, 10 g | N | Parallel | 7 | Y | N | Culture |
| Bouhnik 2007 (55) | 39; 33.9; NR | Inulin, 5 g | A | Sucrose & maltodextrin mix, 5 g | N | Parallel | 28 | Y | Y | Culture |
| Brahe 2015 (59) | 35; 59.6 ³ ; 100% | Flaxseed mucilage, 10 g | G | Placebo | Y | Parallel | 42 | N | N | Quantitative metagenomics qPCR |
| Calame 2008 (60) | 16; 30.9; NR | Arabic gum, 40 g | G | Placebo | Y | Parallel | 28 | N | N | |
| Clarke 2016 (86) | 30; 27; 57% | Beta 2-1 fructan, 15 g | A | Maltodextrin, 15 g | Y | Cross-over | 28 | N | Y | qPCR |
| Cloetens 2010 (87) | 20; 24; 70% | AXOS, 10 g | C | Maltodextrin, 20 g | N | Cross-over | 21 | N | Y | qPCR |
| Costabile 2010 (90) | 31; 25; 56% | Very long chain inulin, 10 g | A | Maltodextrin, 10 g | N | Cross-over | 21 | N | Y | FISH |
| Costabile 2012 (88) | 31; 33; 52% | PDX, 8 g | C | Maltodextrin, 8 g | N | Cross-over | 21 | N | Y | DGGE; FISH |
| Damen 2012 (91) | 27; 25; 63% | AXOS, 2.14 g | C | Placebo | Y | Cross-over | 21 | Y | Y | FISH |
| Depeint 2008 (92) | 30; 36.3; 60% | Beta-GOS, 7 g | A | Sucrose, 7 g | N | Cross-over | 7 | Y | Y | FISH |

| Study | Participants | | Interventions | | | RCT Design | | | | |
|---|---|---|---------------|------------------------|-------------------------|------------|----------------------|--------|----------|-------------------------------|
| | n; age ¹ ; % F | Fiber, daily dose | Prebiotic | Comparator; daily dose | Compliance ² | Design | Duration (days) | Run in | Wash out | Analysis |
| Dewulf 2013 (61) | 30; 47.5; 100% | Inulin-type fructan (Synergy 1), 16 g | A | Maltodextrin, 16 g | N | Parallel | Reported as 3 months | N | N | qPCR; Phylogenetic microarray |
| Elison 2016 (62) | 40; 22-57; 52% | HMO⁶ : 2'-O-fucosyllactose (2'FL); lacto-N-neotetraose (LNnT); Mixture (2:1 mixture of 2'FL + LNnT), 20 g | A | Glucose, 2 g | Y | Parallel | 14 | Y | N | Illumina |
| Fastinger 2008 (63) | 25; 26.7; 50% | Resistant maltodextrin, 15 g | C | Maltodextrin, 15 g | N | Parallel | 21 | Y | Y | qPCR |
| Fernando 2010 (93) | 12; 25.6; 42% | Raffinose, 5 g | G | Placebo | N | Cross-over | 21 | N | N | qPCR; T-RLFP |
| Finegold 2014 (64) | 16; 21-49 ³ ; 66% ³ | XOS, 2.8 g | C | Maltodextrin, 2.8 g | N | Parallel | 56 | Y | Y | Pyrosequencing |
| Francois 2012 (94) | 52; 42; 48% | Wheat bran extract, 10 g | G | Placebo | N | Cross-over | 21 | Y | Y | FISH |
| Fuller 2007 (95); Ramirez-Farias 2009 (50)⁴ | 12; 38.1; 75% | Inulin, 10 g | A | Nil | Y | Cross-over | 16 | N | N | qPCR |
| Gopal 2003 (65) | 19; 20-60 ³ ; 44% ³ | GOS, 2.4 g | A | Placebo | Y | Parallel | 28 | Y | Y | Culture |
| Holscher 2015 (97) | 29; 27; 52% | Agave inulin, 7.5 g | A | Placebo | N | Cross-over | 21 | Y | Y | Illumina |

| Study | Participants | | Interventions | | | RCT Design | | | | |
|----------------------------|--|---|---------------|-----------------------------|-------------------------|------------|-----------------|--------|----------|----------------|
| | n; age ¹ ; % F | Fiber, daily dose | Prebiotic | Comparator; daily dose | Compliance ² | Design | Duration (days) | Run in | Wash out | Analysis |
| Jie 2000 (66) | 30; 29.9; 45% | PDX, 12 g | C | Nil | N | Parallel | 28 | Y | N | Culture |
| Kleesen 2007 (67) | 45; 23.5; 55% | Inulin ⁶ : Chicory inulin; Jerusalem artichoke inulin, 15.4 g | A | Placebo | N | Parallel | 21 | Y | N | Culture; FISH |
| Lecerf 2012 (68) | 59; 20.1; 57% | XOS ⁵ ; Inulin-XOS mix, 6.64 g | C | Wheat dextrin, 6.64 g | N | Parallel | 28 | N | N | qPCR |
| Lin 2016 (69) | 20; 24.2; 80% | XOS, 1.2 g | C | Placebo | N | Parallel | 42 | Y | Y | Culture |
| Lomax 2012 (70) | 43; 55; 74% | Beta 2-1 fructan, 8 g | A | Maltodextrin, 8 g | Y | Parallel | 28 | Y | N | FISH |
| Maki 2012 (99) | 55; 35.1 ³ ; 54% ³ | AXOS, 2.4 g | C | Placebo | N | Cross-over | 21 | N | Y | FISH |
| Maneerat 2013 (100) | 35; 67.4 ³ ; 53% ³ | GOS, 8 g | A | Maltodextrin, 8 g | N | Cross-over | 21 | N | Y | FISH |
| Martinez 2010 (101) | 10; 23-38; 50% | RS ⁶ : RS2; RS4, 33.2 g | C | Native wheat starch, 33.2 g | N | Cross-over | 21 | Y | Y | Pyrosequencing |
| Pallav 2014 (72) | 14; 31.4 ³ ; 65% | Polysaccharidepeptide (I'm-Yunity), 3.6 g | G | Nil | N | Parallel | 14 | N | N | Pyrosequencing |
| Pasman 2006 (73) | 29; 34.1; 0% | Nutriose FB (dextrin), 45 g | A | Maltodextrin, 22.5 g | Y | Parallel | 35 | Y | N | Culture |
| Petry 2012 (102) | 32; 18-40; 100% | Inulin, 20 g | A | Maltodextrin, 20 g | N | Cross-over | 28 | N | Y | qPCR |
| Ramnani 2010 (74) | 66; 32.9; 50% | Inulin, 5 g | A | Placebo | Y | Parallel | 21 | Y | Y | FISH |

| Study | Participants | | Interventions | | | RCT Design | | | | |
|-------------------------------------|--|---------------------------|---------------|------------------------|-------------------------|------------|-----------------|--------|----------|----------|
| | n; age ¹ ; % F | Fiber, daily dose | Prebiotic | Comparator; daily dose | Compliance ² | Design | Duration (days) | Run in | Wash out | Analysis |
| Ramnani 2015 (103) | 38; 35.1 ³ ; 50% | Agave inulin, 5 g | A | Maltodextrin, 5 g | Y | Cross-over | 21 | Y | Y | FISH |
| Salden 2017 (80) | 27; 48; 48% | Arabinoxylans, 15 g | G | Maltodextrin, 15 g | Y | Parallel | 42 | N | N | Illumina |
| Slavin 2011 (105) | 10; 27-49 ³ ; 0% | Chicory inulin, 20 g | A | Placebo | Y | Cross-over | 21 | N | N | Culture |
| Ten Bruggen et al 2006 (107) | 29; 22.7; 0% | FOS, 20 g | A | Sucrose, 6 g | Y | Cross-over | 14 | N | Y | qPCR |
| Tuohy 2011 (108) | NR; NR; 55% | Mix:(FOS & PHGG), 10 g | Mix | Placebo | Y | Cross-over | 21 | N | N | FISH |
| Vulevic 2008 (109) | 41; 69.3 ³ ; 64% ³ | GOS (Bimuno), 5.5 g | A | Maltodextrin, 5.5 g | Y | Cross-over | 70 | N | Y | FISH |
| Vulevic 2015 (110) | 40; 70.4; 62% | GOS (Bimuno), 5.5 g | A | Maltodextrin, 5.5 g | Y | Cross-over | 70 | N | Y | FISH |
| Walton 2010 (113) | 31; 21; 58% | MOS, 5 g | C | Placebo | Y | Cross-over | 21 | N | Y | FISH |
| Walton 2012 (111) | 37; 58.9 ³ ; 57% ³ | GOS, 8 g | A | Placebo | N | Cross-over | 21 | Y | Y | qPCR |
| Walton 2012 (112) | 40; 31.4 ³ ; 60% ³ | AXOS, 2.2 g | C | Placebo | Y | Cross-over | 21 | Y | Y | FISH |
| Wu 2011 (76) | 15; 40.6; 93% | Konjac glucomannan, 4.5 g | G | Nil | N | Parallel | 28 | N | N | FISH |

¹ Age expressed as mean years; age range provided where means were not obtainable. ² Compliance to intervention; assessed by primary study. ³ Refers to randomized population rather than actual population. Compliance to intervention; assessed by primary study. ⁴ Secondary publication reporting additional outcomes from the primary study. ⁵ Refers to analyzed intervention arm with the highest prebiotic classification (accepted prebiotic fiber > candidate prebiotic fiber > general fiber) selected for fiber type subgroup analysis. ⁶ Refers to intervention fibers that have been pooled together for meta-analyses. Abbreviations: A; Accepted prebiotic fiber; AXOS; Arabinoxylan-oligosaccharide; C; Candidate prebiotic fiber; DGGE; Denaturing gradient gel electrophoresis; FISH; Fluorescent *in situ* hybridization; G; General fiber; GOS; Galacto-oligosaccharide; HMO; Human milk oligosaccharide; MOS; Manno-oligosaccharide; NR; Not reported by study; OS; Oligosaccharide; PDX; Polydextrose; PHGG; Partially hydrolyzed guar gum; qPCR; Quantitative polymerase chain reaction; RS; Resistant starch; RS2; Resistant starch 2; RS4; Resistant starch 4; SC-FOS; Short chain fructo-oligosaccharide; TOS; Trans-galacto-oligosaccharide; XOS; Xylo-oligosaccharide.

Table 3: Characteristics of randomized controlled trials of food interventions comparing dietary fiber with low fiber comparators in healthy adults

| Study | Participants | Interventions | | | RCT Design | | | | | | |
|--|------------------------------|----------------------|-----------------------|------------------------|-------------------------|-------------------------|------------|-----------------|--------|----------|----------|
| | n; age ¹ ; % F | Intervention | Comparator | Daily fiber difference | Study diet ² | Compliance ³ | Design | Duration (days) | Run in | Wash out | Analysis |
| Ampatzoglou 2008 (82) | 33; 48.8; 64% | WG diet | RG diet | 10 g | N | Y | Cross-over | 14 | Y | Y | FISH |
| Carvalho-Wells 2010 (85) | 32; 31.6; 66% | WG cereal | Non-WG cereal | 6.5 g | N | N | Cross-over | 21 | Y | Y | FISH |
| Cooper 2017 (78) | 46; 25.8; 46% | WG market basket | RG market basket | 5 g | N | Y | Parallel | 42 | N | N | Illumina |
| Costabile 2008 (89) | 31; 25; 52% | WG cereal | Wheat bran cereal | 7.4 g | N | N | Cross-over | 21 | Y | Y | FISH |
| Grasten 2007 (96) | 14; 59.7 ⁴ ; 100% | Rye bread | White wheat bread | 19 g | N | Y | Cross-over | 56 | Y | Y | Culture |
| Jenkins 1999 (98) | 24; 33; 50% | Wheat bran | Wheat flour | 19 g | N | Y | Cross-over | 14 | N | Y | Culture |
| Karl 2017 (79); Vanegas 2017 (51)⁵ | 81; 40-65 ⁴ ; 60% | WG diet | RG diet | 8 g | Y | Y | Parallel | 42 | Y | N | Illumina |
| Nemoto 2011 (71) | 36; 22-67; 63% | Fermented brown rice | "Non-functional food" | 4.62 g | N | Y | Parallel | 14 | N | N | Culture |
| Ross 2011 | 17; 35; 65% | WG diet | RG diet | 13 g | Y | Y | Cross- | 14 | Y | Y | qPCR |

| Study | Participants | Interventions | | | RCT Design | | | | | | |
|------------------|---------------------------|--------------------------|----------------|------------------------|-------------------------|-------------------------|------------|-----------------|--------|----------|--------------------|
| | n; age ¹ ; % F | Intervention | Comparator | Daily fiber difference | Study diet ² | Compliance ³ | Design | Duration (days) | Run in | Wash out | Analysis |
| (104) | | | | | | | over | | | | |
| Smith 2006 (106) | 18; 42.8; 0% | Lupin kernal fiber diet | Control diet | 22 g | Y | N | Cross-over | 28 | N | Y | FISH |
| Tap 2015 (75) | 19; 19-25; 53% | High fiber diet | Low fiber diet | 30 g | Y | Y | Cross-over | 5 | N | Y | 454 Pyrosequencing |
| Zeng 2015 (114) | 77; 63.4; 70% | Whole cereal legume diet | Control diet | 14.5 g | Y | Y | Parallel | 90 | N | N | Culture |

¹ Age expressed as mean years; age range provided where means were not obtainable. ² Whether the participant's entire diet was provided by the study. ³ Compliance to intervention; assessed by primary study. ⁴ Refers to randomized population rather than actual population. ⁵ Secondary publication reporting additional outcomes from the primary study. Abbreviations: FISH; Fluorescent *in situ* hybridization; qPCR; Quantitative polymerase chain reaction; RG; Refined grain; WG; Whole grain.

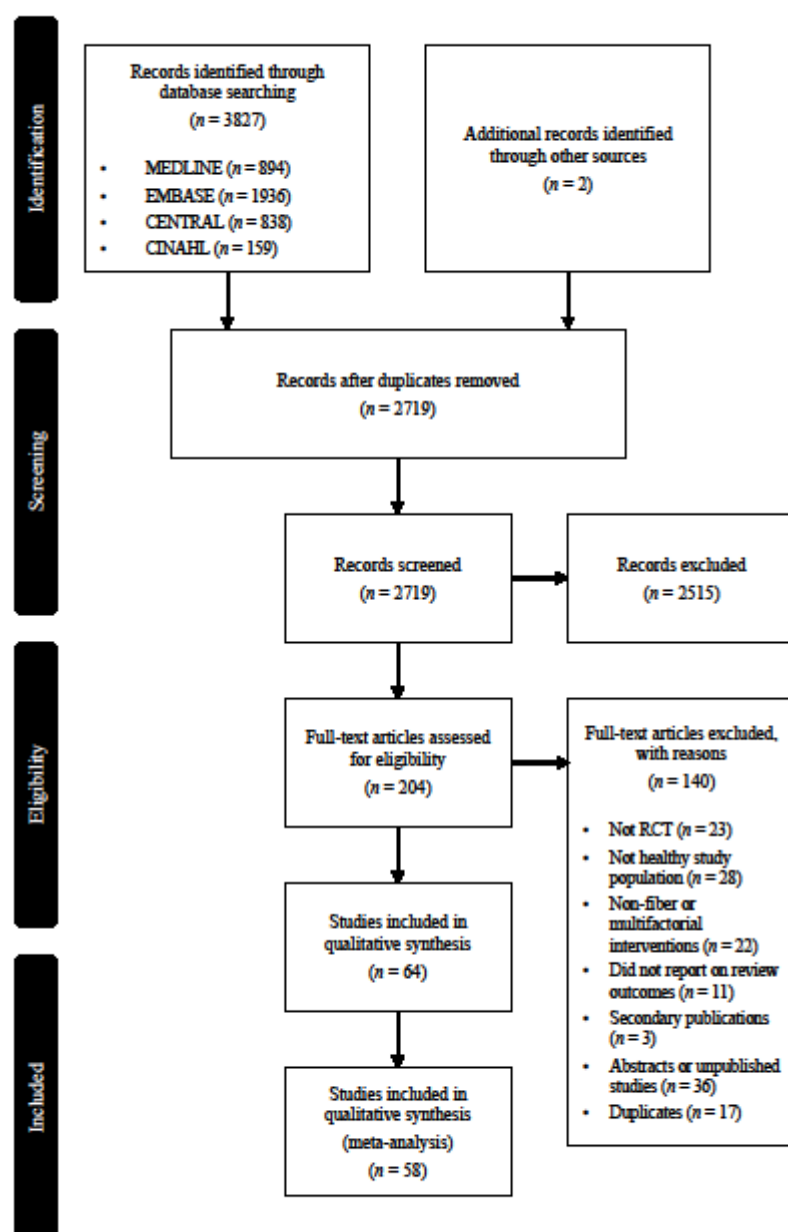


Figure 1: Flow diagram of studies evaluated in the systematic review.

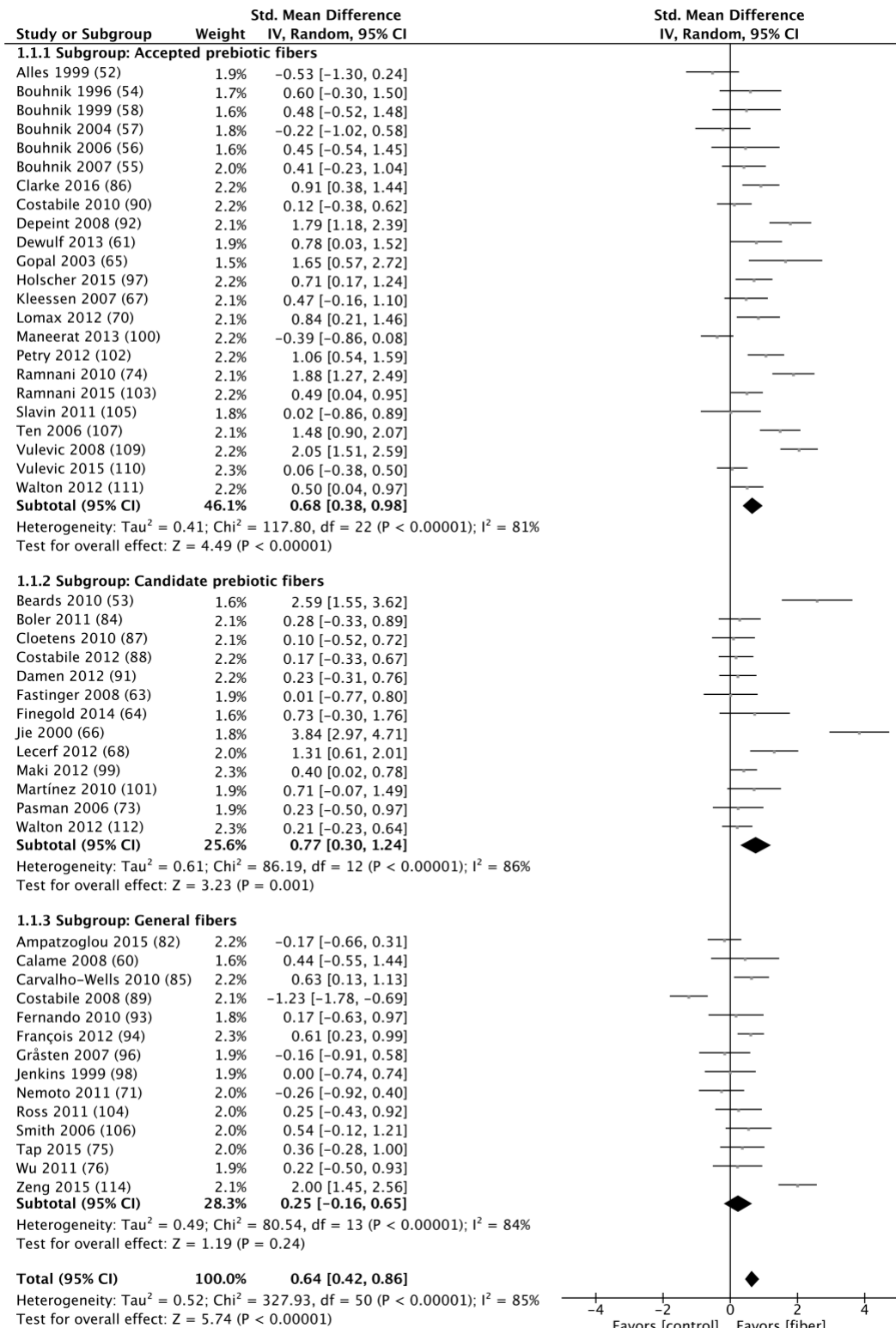


Figure 2: Forest plot of randomized controlled trials in healthy adults comparing dietary fiber with placebo/low fiber comparators. Studies are sub-grouped by fiber type, with the overall effect included at the bottom. Data are presented as means and SDs of *Bifidobacterium* spp. abundance at end of intervention. Effects of trials are presented as weights (percentages) and SMD (95% CI). CI, confidence interval; IV, inverse variance; SD, standard deviation; SMD, standardized mean difference.

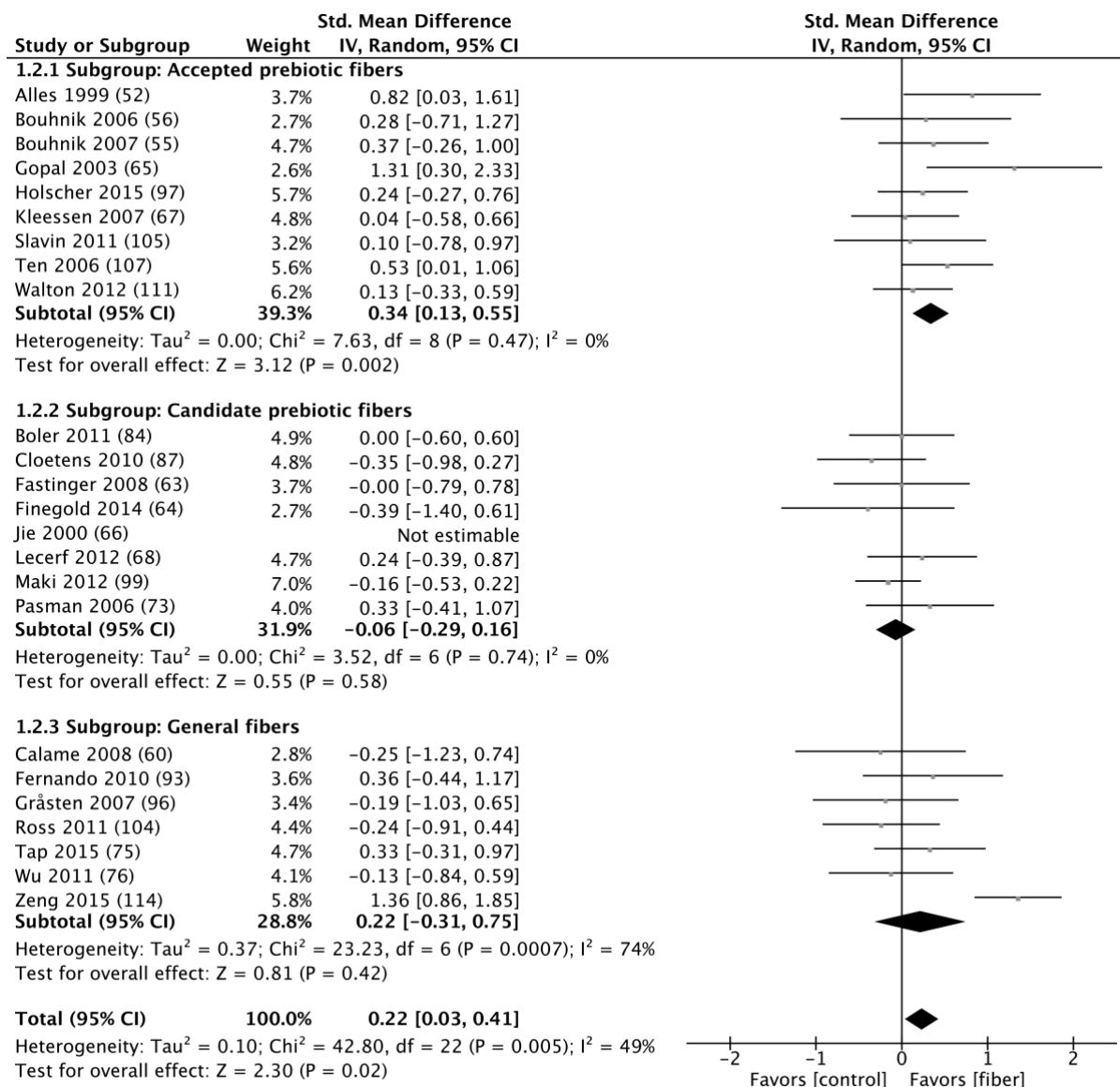


Figure 3: Forest plot of randomized controlled trials in healthy adults comparing dietary fiber with placebo/low fiber comparators. Studies are sub-grouped by fiber type, with the overall effect included at the bottom. Data are presented as means and SDs of *Lactobacillus* spp. abundance at end of intervention are reported for trials. Effects of trials are presented as weights (percentages) and SMD (95% CI). CI, confidence interval; IV, inverse variance; SD, standard deviation; SMD, standardized mean difference.

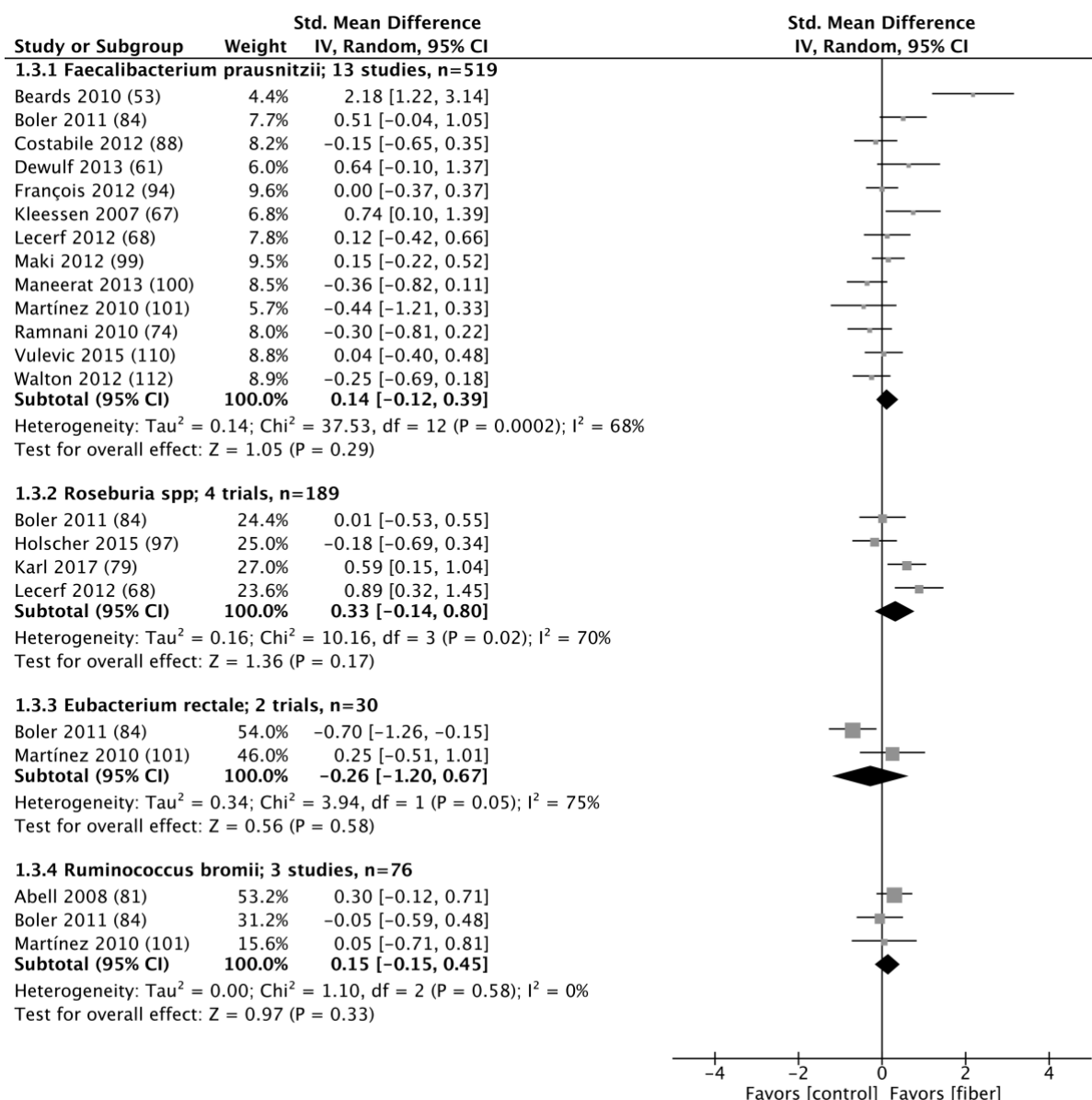


Figure 4: Forest plot of randomized controlled trials in healthy adults comparing dietary fiber with placebo/low fiber comparators. The means and SDs of *Faecalibacterium prausnitzii*, *Roseburia* spp., *Eubacterium rectale* and *Ruminococcus bromii* abundance at end of intervention are reported for trials. Effects of trials are presented as weights (percentages) and SMD (95% CI). CI, confidence interval; IV, inverse variance; SD, standard deviation; SMD, standardized mean difference.

Supplemental Table 1: Search algorithm: MEDLINE via OVID

Supplemental Table 2: Search algorithm: EMBASE

Supplemental Table 3: Search algorithm: CENTRAL

Supplemental Table 4: Search algorithm: CINAHL

Supplemental Table 5: Reasons for excluding studies from full text analysis

Supplemental Table 6: Outcomes of pre-defined subgroup analyses undertaken

Supplemental Table 7: Outcomes of post hoc subgroup analyses undertaken

Supplemental Figure 1: Risk of bias across the included studies showing the summary percentage in each domain

Supplemental Figure 2: Funnel plot for the effect of dietary fiber on *Bifidobacterium* spp. abundance

Supplemental Figure 3: Funnel plot for the effect of dietary fiber on *Lactobacillus* spp. abundance

Supplemental Figure 4: Funnel plot for the effect of dietary fiber on total fecal SCFA

Supplemental Figure 5: Funnel plot for the effect of dietary fiber on fecal acetate

Supplemental Figure 6: Funnel plot for the effect of dietary fiber on fecal propionate

Supplemental Figure 7: Funnel plot for the effect of dietary fiber on fecal butyrate

Supplemental Table 1: Search algorithm: MEDLINE via OVID

| | |
|---|--|
| 1. exp Dietary Fiber/ | 46. exp Inulin/ |
| 2. roughage*.tw. | 47. Inulin*.tw. |
| 3. exp Prebiotics/ | 48. (gentiooligosaccharide* or gentio- oligosaccharide*).tw. |
| 4. prebiotic*.tw. | 49. (isomalto oligosaccharide* or isomalto- oligosaccharide* or imo).tw. |
| 5. (carbohydrate adj2 polymer*).tw. | 50. (mannanoligosaccharide* or mannano- oligosaccharide*).tw. |
| 6. ((non-starch or nonstarch) adj (poly-saccharide* or polysaccharide*)).tw. | 51. (N-acetylchitooligosaccharide* or N-acetylchito- oligosaccharide*).tw. |
| 7. 1 or 2 or 3 or 4 or 5 or 6 | 52. (pectic oligosaccharide* or pectic- oligosaccharide*).tw. |
| 8. Diet/ | 53. (resistant starch* or resistant-starch*).tw. |
| 9. diet*.tw. | |
| 10. consum*.tw. | |
| 11. eat*.tw. | |
| 12. food*.tw. | |
| 13. nutri*.tw. | |
| 14. 8 or 9 or 10 or 11 or 12 or 13 | 54. (soybean oligosaccharide* or soybean- oligosaccharide*).tw. |
| 15. Agar/ | 55. (xylooligosaccharide* or xylo- oligosaccharide*).tw. |
| 16. agar*.tw. | 56. exp Oligosaccharides/ |
| 17. Alginates/ | 57. Oligosaccharide*.tw. |
| 18. alginate*.tw. | 58. (fiber* or fiber* or high-fiber* or high-fiber*).tw. |
| 19. (alginic adj2 acid*).tw. | 59. 15 or 16 or 17 or 18 or 19 or 20 or 21 or 22 or 23 or 24 or 25 or 26 or 27 or 28 or 29 or 30 or 31 or 32 or 33 or 34 or 35 or 36 or 37 or 38 or 39 or 40 or 41 or 42 or 43 or 44 or 45 or 46 or 47 or 48 or 49 or 50 or 51 or 52 or 53 or 54 or 55 or 56 or 57 or 58 |
| 20. Carrageenan/ | |
| 21. carrageen*.tw. | 60. 14 and 59 |
| 22. exp Cellulose/ | 61. 7 or 60 |
| 23. cellulose*.tw. | 62. exp Gastrointestinal Microbiome/ |
| 24. exp Chitin/ | 63. (microbiota or microbiome).tw. |
| 25. chitin*.tw. | 64. bifido*.tw. |
| 26. hemicellulose*.tw. | 65. lactobacill*.tw. |
| 27. hexosan*.tw. | 66. 62 or 63 or 64 or 65 |
| 28. Lignin/ | 67. (faecal or fecal).tw. |
| 29. lignin*.tw. | 68. (bacteri* or flora).tw. |
| 30. Pectins/ | 69. 67 and 68 |
| 31. pectin*.tw. | 70. exp Dysbiosis/ |
| 32. pentosan*.tw. | 71. 66 or 69 or 70 |
| 33. polydextrose*.tw. | 72. 61 and 71 |
| 34. polyuronide*.tw. | 73. ((randomized controlled trial or controlled clinical trial).pt. or randomized.ab. or randomised.ab. or placebo.ab. or drug therapy.fs. or randomly.ab. or trial.ab. or groups.ab.) not (exp animals/ not humans.sh.) |
| 35. Raffinose/ | 74. 72 and 73 |
| 36. raffinose*.tw. | |
| 37. xanthan*.tw. | |
| 38. Xylose/ | |
| 39. xylose*.tw. | |
| 40. exp Galactans/ | |
| 41. galactan*.tw. | |
| 42. (galactooligosaccharide* or galacto- oligosaccharide* or gos or tos).tw. | |
| 43. exp Fructans/ | |
| 44. fructan*.tw. | |
| 45. (fructooligosaccharide* or fructo- oligosaccharide* or fos or oligofructose or oligo- fructose).tw. | |

Supplemental Table 2: Search algorithm: EMBASE

| | |
|--|--|
| 1. exp Dietary Fiber/ | 46. exp Inulin/ |
| 2. roughage*.tw. | 47. Inulin*.tw. |
| 3. exp Prebiotics/ | 48. (gentiooligosaccharide* or gentio- |
| 4. prebiotic*.tw. | oligosaccharide*).tw. |
| 5. (carbohydrate adj2 polymer*).tw. | 49. (isomalto oligosaccharide* or isomalto- |
| 6. ((non-starch or nonstarch) adj (poly-saccharide* or | oligosaccharide* or imo).tw. |
| polysaccharide*)).tw. | 50. (mannanoligosaccharide* or mannano- |
| 7. 1 or 2 or 3 or 4 or 5 or 6 | oligosaccharide*).tw. |
| 8. Diet/ | 51. (N-acetylchitooligosaccharide* or N-acetylchito- |
| 9. diet*.tw. | oligosaccharide*).tw. |
| 10. consum*.tw. | 52. (pectic oligosaccharide* or pectic- |
| 11. eat*.tw. | oligosaccharide*).tw. |
| 12. food*.tw. | 53. (resistant starch* or resistant-starch*).tw. |
| 13. nutri*.tw. | 54. (soybean oligosaccharide* or soybean- |
| 14. 8 or 9 or 10 or 11 or 12 or 13 | oligosaccharide*).tw. |
| 15. Agar/ | 55. (xylooligosaccharide* or xylo- |
| 16. agar*.tw. | oligosaccharide*).tw. |
| 17. Alginates/ | 56. exp Oligosaccharides/ |
| 18. alginate*.tw. | 57. Oligosaccharide*.tw. |
| 19. (alginic adj2 acid*).tw. | 58. (fiber* or fiber* or high-fiber* or high-fiber*).tw. |
| 20. Carrageenan/ | 59. 15 or 16 or 17 or 18 or 19 or 20 or 21 or 22 or 23 |
| 21. carrageen*.tw. | or 24 or 25 or 26 or 27 or 28 or 29 or 30 or 31 or 32 |
| 22. exp Cellulose/ | or 33 or 34 or 35 or 36 or 37 or 38 or 39 or 40 or 41 |
| 23. cellulose*.tw. | or 42 or 43 or 44 or 45 or 46 or 47 or 48 or 49 or 50 |
| 24. exp Chitin/ | or 51 or 52 or 53 or 54 or 55 or 56 or 57 or 58 |
| 25. chitin*.tw. | |
| 26. hemicellulose*.tw. | 60. 14 and 59 |
| 27. hexosan*.tw. | 61. 7 or 60 |
| 28. Lignin/ | 62. exp Gastrointestinal Microbiome/ |
| 29. lignin*.tw. | 63. (microbiota or microbiome).tw. |
| 30. Pectins/ | 64. bifido*.tw. |
| 31. pectin*.tw. | 65. lactobacill*.tw. |
| 32. pentosan*.tw. | 66. 62 or 63 or 64 or 65 |
| 33. polydextrose*.tw. | 67. (faecal or fecal).tw. |
| 34. polyuronide*.tw. | 68. (bacteri* or flora).tw. |
| 35. Raffinose/ | 69. 67 and 68 |
| 36. raffinose*.tw. | 70. exp Dysbiosis/ |
| 37. xanthan*.tw. | 71. 66 or 69 or 70 |
| 38. Xylose/ | 72. 61 and 71 |
| 39. xylose*.tw. | 73. ((randomized controlled trial or controlled |
| 40. exp Galactans/ | clinical trial).pt. or randomized.ab. or randomised.ab. |
| 41. galactan*.tw. | or placebo.ab. or drug therapy.fs. or randomly.ab. or |
| 42. (galactooligosaccharide* or galacto- | trial.ab. or groups.ab.) not (exp animals/ not |
| oligosaccharide* or gos or tos).tw. | humans.sh.) |
| 43. exp Fructans/ | 74. 72 and 73 |
| 44. fructan*.tw. | |
| 45. (fructooligosaccharide* or fructo- | |
| oligosaccharide* or fos or oligofructose or oligo- | |
| fructose).tw. | |

Supplemental Table 3: Search algorithm: CENTRAL

| | | | |
|----------------------------------|--|---|--|
| #1 | MeSH descriptor: [Dietary Fiber] | #40 | MeSH descriptor: [Galactans] explode all trees |
| explode all trees | | #41 | galactan* |
| #2 | roughage* | #42 | (galactooligosaccharide* or galacto- |
| #3 | MeSH descriptor: [Prebiotics] explode | oligosaccharide* or gos or tos) | |
| all trees | | #43 | MeSH descriptor: [Fructans] explode all trees |
| #4 | prebiotic* | #44 | fructan* |
| #5 | carbohydrate near/2 polymer* | #45 | (fructooligosaccharide* or fructo- |
| #6 | ((non-starch or nonstarch) near (poly- | oligosaccharide* or fos or oligofructose* or oligo- | |
| saccharide* or polysaccharide*)) | | fructose*) | |
| #7 | #1 or #2 or #3 or #4 or #5 or #6 | #46 | MeSH descriptor: [Inulin] explode all trees |
| #8 | MeSH descriptor: [Diet] this term only | #47 | inulin* |
| #9 | diet* | #48 | (gentiooligosaccharide* or gentio- |
| #10 | consum* | oligosaccharide*) | |
| #11 | eat* | #49 | (isomalto oligosaccharide* or isomalto- |
| #12 | food* | oligosaccharide* or imo) | |
| #13 | nutri* | #50 | (mannanooligosaccharide* or mannano- |
| #14 | #8 or #9 or #10 or #11 or #12 or #13 | oligosaccharide*) | |
| #15 | MeSH descriptor: [Agar] this term | #51 | (N-acetylchitooligosaccharide* or N-acetylchito- |
| only | | oligosaccharide*) | |
| #16 | agar* | #52 | (pectic oligosaccharide* or pectic- |
| #17 | MeSH descriptor: [Alginates] this term | oligosaccharide*) | |
| only | | #53 | (resistant starch* or resistant-starch*) |
| #18 | alginate* | #54 | (soybean oligosaccharide* or soybean- |
| #19 | alginic near/2 acid | oligosaccharide*) | |
| #20 | MeSH descriptor: [Carrageenan] this | #55 | (xylooligosaccharide* or xylo-oligosaccharide*) |
| term only | | #56 | MeSH descriptor: [Oligosaccharides] explode all |
| #21 | carrageen* | trees | |
| #22 | MeSH descriptor: [Cellulose] explode | #57 | oligosaccharide* |
| all trees | | #58 | fiber* or fiber* or high-fiber* or high-fiber* |
| #23 | cellulose* | #59 | #15 or #16 or #17 or #18 or #19 or #20 or #21 or |
| #24 | MeSH descriptor: [Chitin] explode all | #22 or #23 or #24 or #25 or #26 or #27 or #28 or #29 or | |
| trees | | #30 or #31 or #32 or #33 or #34 or #35 or #36 or #37 or | |
| #25 | chitin* | #38 or #39 or #40 or #41 or #42 or #43 or #44 or #45 or | |
| #26 | hemicellulose* | #46 or #47 or #48 or #49 or #50 or #51 or #51 or #52 or | |
| #27 | hexosan* | #53 or #54 or #55 or #56 or #56 or #57 or #58 | |
| #28 | MeSH descriptor: [Lignin] this term | #60 | #14 and #59 |
| only | | #61 | #7 or #60 |
| #29 | lignin* | #62 | MeSH descriptor: [Gastrointestinal Microbiome] |
| #30 | MeSH descriptor: [Pectins] this term | explode all trees | |
| only | | #63 | (microbiota or microbiome) |
| #31 | pectin* | #64 | bifido* |
| #32 | pentosan* | #65 | lactobacill* |
| #33 | polydextrose* | #66 | #62 or #63 or #64 or #65 |
| #34 | polyuronide* | #67 | (faecal or fecal) |
| #35 | MeSH descriptor: [Raffinose] this term | #68 | (bacteri* or flora) |
| only | | #69 | #67 and #68 |
| #36 | raffinose* | #70 | MeSH descriptor: [Dysbiosis] explode all trees |
| #37 | xanthan* | #71 | #66 or #69 or #70 |
| #38 | MeSH descriptor: [Xylose] this term | #72 | #61 and #71 |
| only | | | |
| #39 | xylose* | | |

Supplemental Table 4: Search algorithm: CINAHL

1. ((dietary fib* OR roughage* OR prebiotic*) OR (diet* OR consum* OR eat* OR food* OR nutri*) AND (agar* OR alginate* OR carrageen* OR cellulose* OR chitin* OR hemicellulose* OR hexosan* OR lignin* OR pectin* OR pentosan* OR polydextrose* OR polyuronide* OR raffinose* OR xanthan* OR xylose* OR galactan* OR galactooligosaccharide* OR galacto-oligosaccharide* OR gos OR tos OR fructan* OR fructooligosaccharide* OR fructo-oligosaccharide* OR fos OR oligofructose* OR oligo-fructose* OR inulin* OR gentiooligosaccharide* OR gentio-oligosaccharide* OR isomalto oligosaccharide* OR isomalto-oligosaccharide* OR imo OR mannanooligosaccharide* OR mannano-oligosaccharide* OR N-acetylchitooligosaccharide* OR N-acetylchito-oligosaccharide* OR pectic oligosaccharide* OR pectic-oligosaccharide* OR resistant starch* OR resistant-starch* OR soybean oligosaccharide* OR soybean-oligosaccharide* OR oligosaccharide* OR high-fib*))
2. ((MH "Microbiota") OR microbiota OR microbiome OR bifido* OR lactobacill*) OR ((faecal OR fecal) AND (bacteri* OR flora)) OR (dysbio*)
3. (MH "Clinical Trials+") OR (MH "Quantitative Studies") OR TI placebo* OR AB placebo* OR (MH "Placebos") OR (MH "Random Assignment") OR TI random* OR AB random* OR TI ((singl* or doubl* or tripl* or trebl*) W1 (blind* or mask*)) OR AB ((singl* or doubl* or tripl* or trebl*) W1 (blind* or mask*)) OR TI clinic* trial* OR AB clinic* trial* OR PT clinical trial

Supplemental Table 5: Reasons for excluding studies following full text analysis*

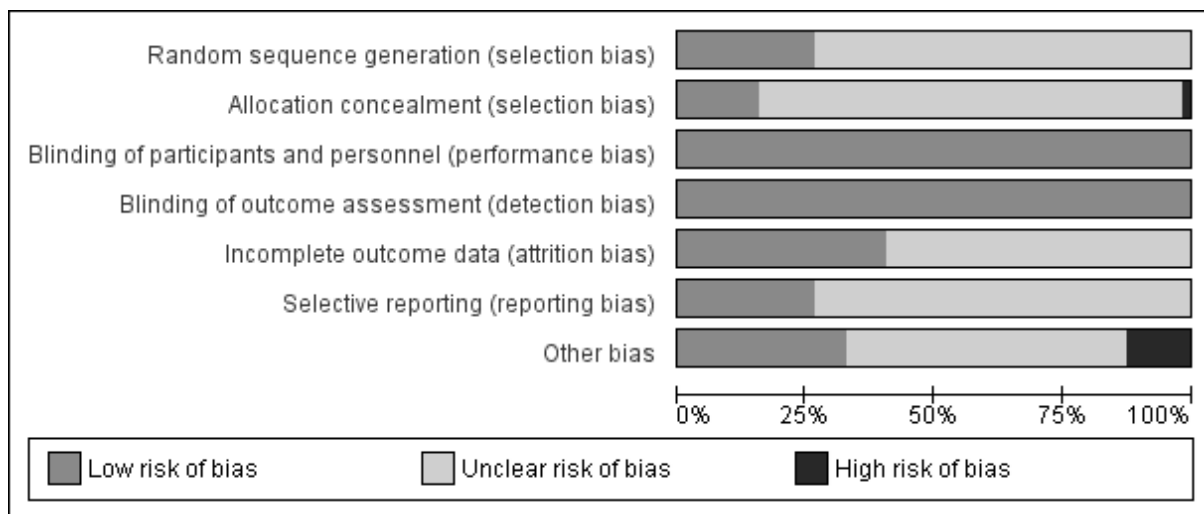
| Study Citation | Reason for exclusion |
|-------------------------|--|
| Nil author 2013 (1) | Not RCT |
| Alfa 2017 (2) | Duplicate |
| Azcarate-Peril 2013 (3) | Not healthy study population |
| Azcarate-Peril 2016 (4) | Not healthy study population |
| Azcarate-Peril 2017 (5) | Not healthy study population |
| Azpiroz 2016 (6) | Not healthy study population |
| Baer 2009 (7) | Abstracts or unpublished studies |
| Benus 2010 (8) | Non-fiber or multifactorial intervention |
| Brahe 2014 (9) | Duplicate |
| Breinholt 2005 (10) | Non-fiber or multifactorial intervention |
| Brighenti 1999 (11) | Not RCT |
| Casellas 2007 (12) | Not healthy study population |
| Chen 2006 (13) | Not RCT |
| Chen 2008 (14) | Not healthy study population |
| Christensen 2013 (15) | Non-fiber or multifactorial intervention |
| Chung 2007 (16) | Not RCT |
| Clarke 2016 (17) | Duplicate |
| Clarke 2016 (18) | Duplicate |
| Clarke 2016 (19) | Duplicate |
| Cooper 2016 (20) | Abstracts or unpublished studies |
| Costabile 2016 (21) | Not RCT |
| Culpepper 2012 (22) | Abstracts or unpublished studies |
| Davis 2010 (23) | Not RCT |
| Davis 2011 (24) | Not RCT |
| De Preter 2007 (25) | Not RCT |
| Demircioglu 2008 (26) | Non-fiber or multifactorial intervention |
| Dewulf 2011 (27) | Abstracts or unpublished studies |
| Dewulf 2012 (28) | Abstracts or unpublished studies |
| Eastwood 1995 (29) | Non-fiber or multifactorial intervention |
| Eid 2015 (30) | Non-fiber or multifactorial intervention |
| Elison 2016 (31) | Duplicate |
| Famdodu 2016 (32) | Abstracts or unpublished studies |
| Famodu 2016 (33) | Abstracts or unpublished studies |
| Fava 2013 (34) | Non-fiber or multifactorial intervention |
| Finley 2007 (35) | Did not report on review outcomes |
| Ford 2017 (36) | Abstracts or unpublished studies |
| Gopal 2003 (37) | Duplicate |
| Gordon 2017 (38) | Abstracts or unpublished studies |
| Grasten 2000 (39) | Did not report on review outcomes |
| Guetterman 2016 (40) | Non-fiber or multifactorial intervention |
| Guglielmetti 2013 (41) | Non-fiber or multifactorial intervention |
| Hald 2016 (42) | Not healthy study population |
| Halmos 2013 (43) | Duplicate |
| Halmos 2014 (44) | Not healthy study population |
| Halmos 2015 (45) | Duplicate |
| Healey 2016 (46) | Abstracts or unpublished studies |
| Heiman 2014 (47) | Not healthy study population |
| Holscher 2014 (48) | Duplicate |
| Holscher 2015 (49) | Abstracts or unpublished studies |
| Hooda 2012 (50) | Secondary publication |
| Jalanka 2016 (51) | Abstracts or unpublished studies |
| Jenkins 1999 (52) | Did not report on review outcomes |
| Karl 2017 (53) | Duplicate |
| Kellow 2014 (54) | Not healthy study population |
| Klinder 2016 (55) | Non-fiber or multifactorial intervention |

| Study Citation | Reason for exclusion |
|-------------------------------|--|
| Klosterbuer 2013 (56) | Did not report on review outcomes |
| Kolida 2007 (57) | Not RCT |
| Kovatcheva-Datchary 2015 (58) | Did not report on review outcomes |
| Kruse 1999 (59) | Not RCT |
| Lambert 2014 (60) | Abstracts or unpublished studies |
| Lambert 2015 (61) | Not healthy study population |
| Lamichhane 2014 (62) | Did not report on review outcomes |
| Langlands 2004 (63) | Not RCT |
| Lappi 2013 (64) | Not healthy study population |
| Lee 2016 (65) | Did not report on review outcomes |
| Lehtinen 2012 (66) | Abstracts or unpublished studies |
| Li 2009 (67) | Non-fiber or multifactorial intervention |
| Li 2014 (68) | Abstracts or unpublished studies |
| Li 2015 (69) | Abstracts or unpublished studies |
| Lin 2014 (70) | Not healthy study population |
| Lin 2016 (71) | Duplicate |
| Linetzky 2012 (72) | Not healthy study population |
| Lomax 2012 (73) | Duplicate |
| Lomax 2013 (74) | Duplicate |
| Lomax 2013 (75) | Abstracts or unpublished studies |
| Mai 2009 (76) | Abstracts or unpublished studies |
| Mai 2012 (77) | Non-fiber or multifactorial intervention |
| Maki 2011 (78) | Abstracts or unpublished studies |
| Marteau 2011 (79) | Not healthy study population |
| Matthan 2015 (80) | Abstracts or unpublished studies |
| Mayengbam 2017 (81) | Abstracts or unpublished studies |
| Medina-Vera 2017 (82) | Abstracts or unpublished studies |
| Mego 2017 (83) | Non-fiber or multifactorial intervention |
| Mitchell 2015 (84) | Not healthy study population |
| Mitsou 2009 (85) | Non-fiber or multifactorial intervention |
| Mitsou 2011 (86) | Non-fiber or multifactorial intervention |
| Orrhage 2000 (87) | Non-fiber or multifactorial intervention |
| Pantophlet 2017 (88) | Not RCT |
| Ramirez-Farias 2009 (89) | Secondary publication |
| Ramprasath 2015 (90) | Abstracts or unpublished studies |
| Rao 2001 (91) | Not RCT |
| Ravn-Haren 2013 (92) | Non-fiber or multifactorial intervention |
| Robinson 2001 (93) | Not RCT |
| Salazar 2013 (94) | Abstracts or unpublished studies |
| Salazar 2015 (95) | Abstracts or unpublished studies |
| Salden 2015 (96) | Abstracts or unpublished studies |
| Salonen 2014 (97) | Not healthy study population |
| Scarpellini 2012 (98) | Abstracts or unpublished studies |
| Scarpellini 2016 (99) | Did not report on review outcomes |
| Scholtens 2006 (100) | Did not report on review outcomes |
| Sloan 2016 (101) | Abstracts or unpublished studies |
| Smilowitz 2017 (102) | Not RCT |
| Song 2015 (103) | Non-fiber or multifactorial intervention |
| Souza 2015 (104) | Not healthy study population |
| Surakka 2009 (105) | Not healthy study population |
| Tannock 2004 (106) | Not RCT |
| Taylor 2016 (107) | Non-fiber or multifactorial intervention |
| Thompson 2016 (108) | Abstracts or unpublished studies |
| Thompson 2016 (109) | Abstracts or unpublished studies |
| Tomono 2010 (110) | Not healthy study population |
| Tuohy 2001 (111) | Not RCT |
| Tuohy 2001 (112) | Duplicate |

| Study Citation | Reason for exclusion |
|-------------------------|--|
| Ukhanova 2014 (113) | Non-fiber or multifactorial intervention |
| Upadhyaya 2016 (114) | Not healthy study population |
| Vanegas 2016 (115) | Abstracts or unpublished studies |
| Vanegas 2017 (116) | Secondary publication |
| Vanegas 2017 (117) | Duplicate |
| Vendrame 2011 (118) | Non-fiber or multifactorial intervention |
| Venkataraman 2016 (119) | Not RCT |
| Vitaglione 2015 (120) | Non-fiber or multifactorial intervention |
| Vulevic 2013 (121) | Not healthy study population |
| Walker 2011 (122) | Not healthy study population |
| Wallace 2015 (123) | Not RCT |
| Weickert 2011 (124) | Not healthy study population |
| West 2012 (125) | Not RCT |
| Westreich 2017 (126) | Abstracts or unpublished studies |
| Whisner 2016 (127) | Not healthy study population |
| Willis 2013 (128) | Did not report on review outcomes |
| Windey 2015 (129) | Did not report on review outcomes |
| Wong 2010 (130) | Not RCT |
| Wood 2017 (131) | Abstracts or unpublished studies |
| Wood 2017 (132) | Abstracts or unpublished studies |
| Worthley 2009 (133) | Not RCT |
| Worthley 2009 (134) | Abstracts or unpublished studies |
| Wutzke 2012 (135) | Abstracts or unpublished studies |
| Xiao 2014 (136) | Not RCT |
| Yang 2015 (137) | Not healthy study population |
| Yen 2011 (138) | Duplicate |
| Yen 2011 (139) | Not healthy study population |
| Yen 2011 (140) | Not healthy study population |

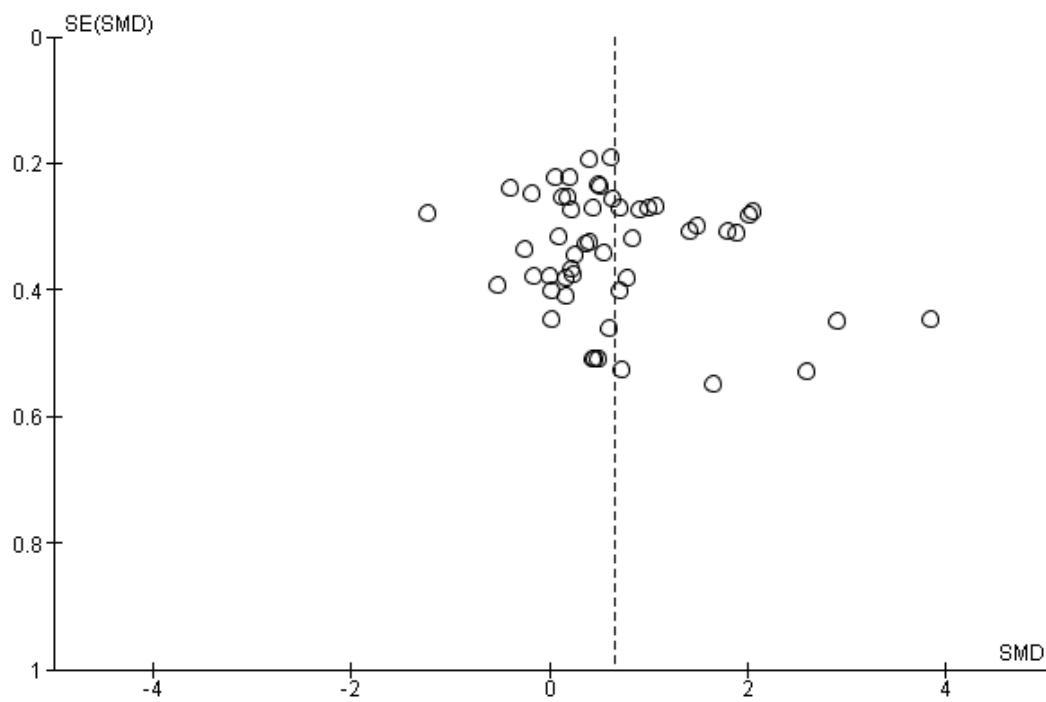
* Citation numbers do not correspond to citations in main manuscript, and are provided at the end of this document.

Risk of Bias

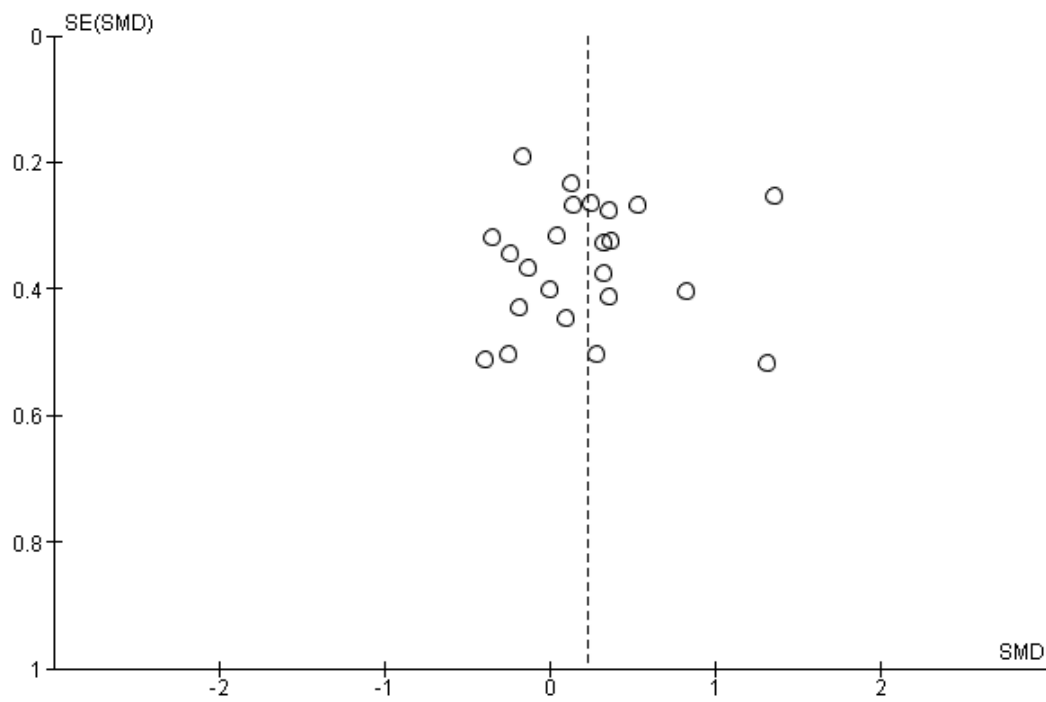


Supplemental Figure 1: Risk of bias across the included studies showing the summary percentage in each domain

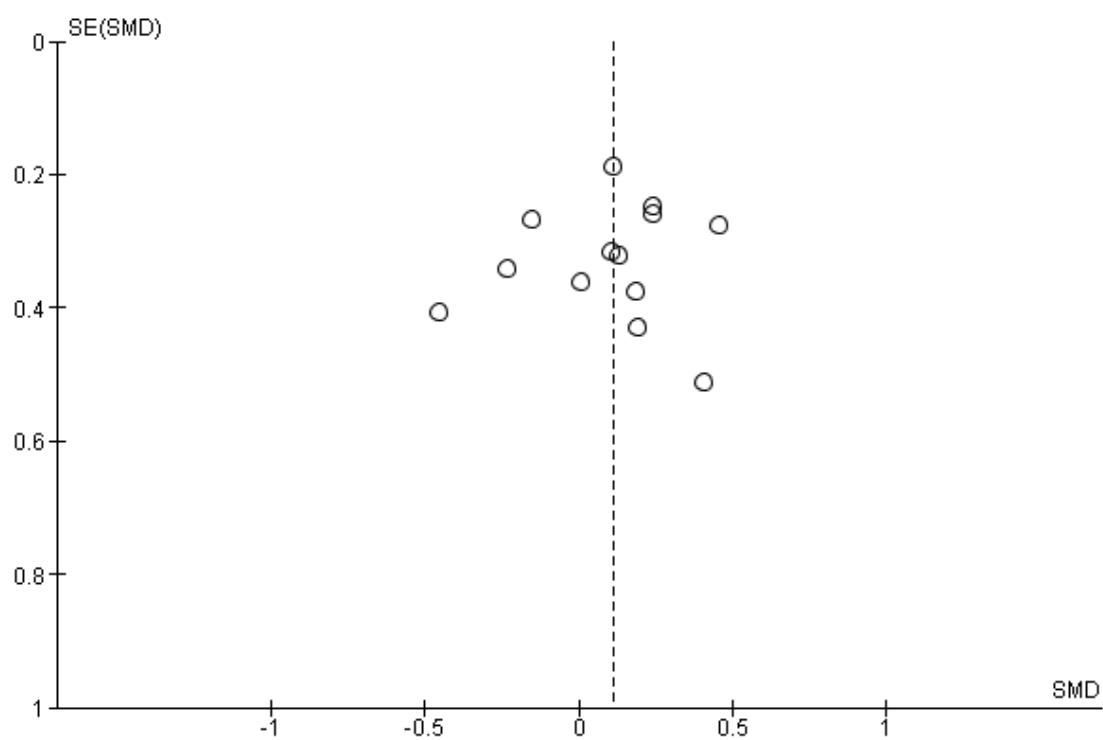
Reporting Bias



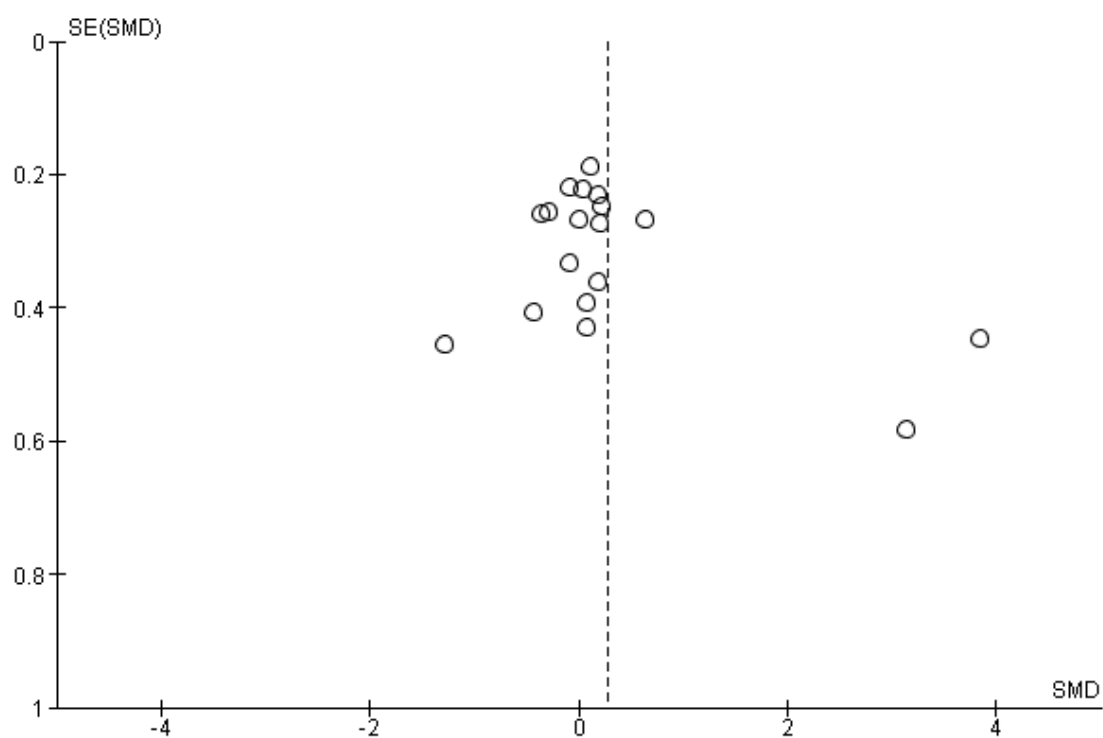
Supplemental Figure 2: Funnel plot for the effect of dietary fiber on *Bifidobacterium* spp. abundance



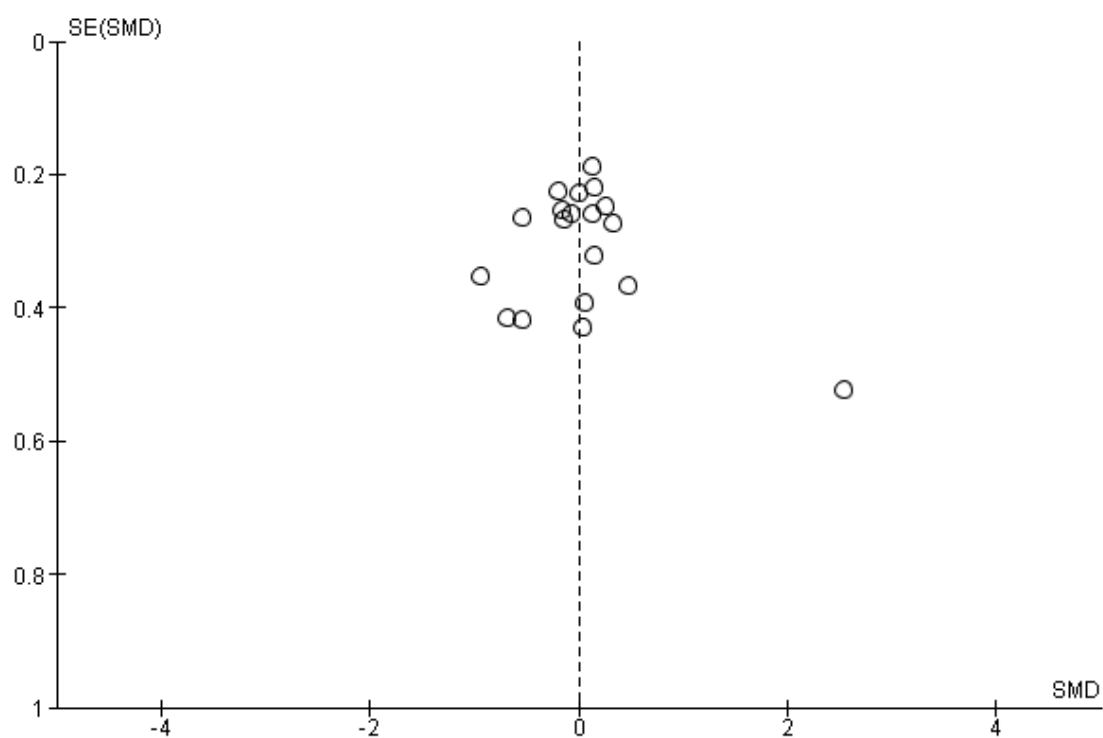
Supplemental Figure 3: Funnel plot for the effect of dietary fiber on *Lactobacillus* spp. abundance



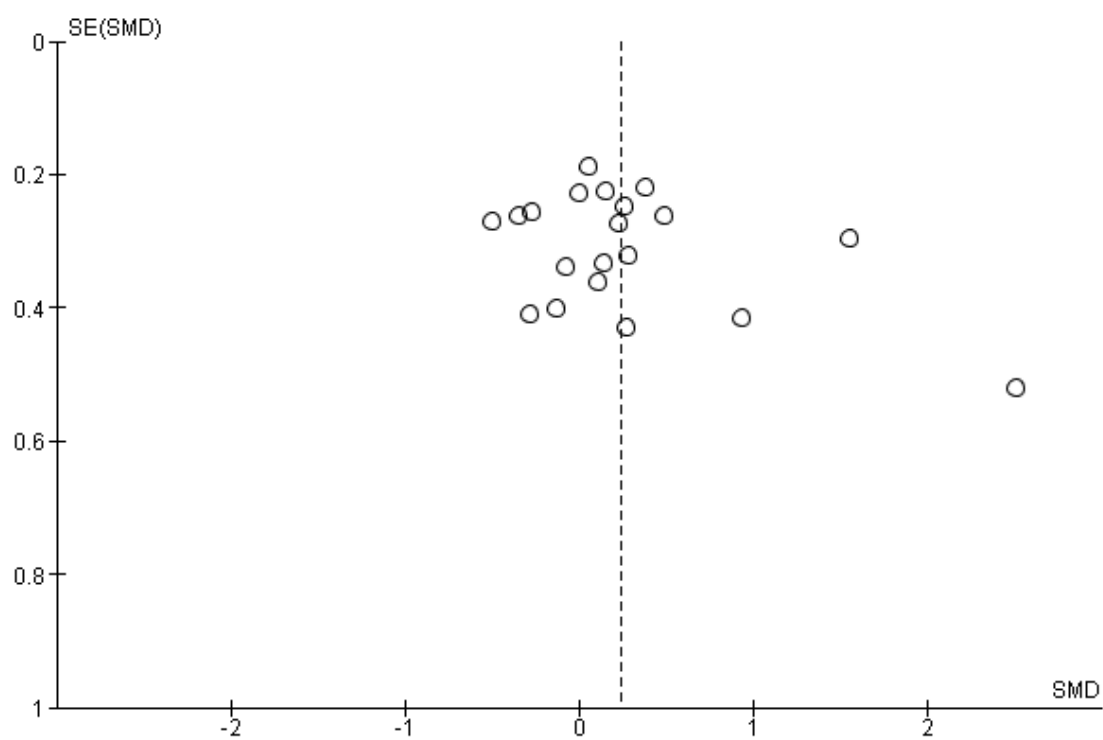
Supplemental Figure 4: Funnel plot for the effect of dietary fiber on total fecal SCFA



Supplemental Figure 5: Funnel plot for the effect of dietary fiber on fecal acetate



Supplemental Figure 6: Funnel plot for the effect of dietary fiber on fecal propionate



Supplemental Figure 7: Funnel plot for the effect of dietary fiber on fecal butyrate

Supplemental Table 6: Outcomes of pre-defined subgroup analyses undertaken

| Outcome | Subgroup analysis | Subgroup difference (I ²) | Subgroups | Studies in subgroup (n) | Result | P | Heterogeneity | | |
|-----------------------------|-------------------|---------------------------------------|---------------------|-------------------------|---|----------|------------------|----------|----------------|
| | | | | | Meta-analysis overall estimate (95% CI) | | Chi-squared test | P | I ² |
| Shannon Diversity Index | Trial design | 0% | Cross-over | 3 | MD: -0.10 (95% CI: -0.19, -0.01) | 0.03 | 1.36 | 0.51 | 0% |
| | | | Parallel | 3 | MD: -0.03 (95% CI: -0.57, 0.51) | 0.91 | 9.35 | 0.009 | 79% |
| <i>Bifidobacterium</i> spp. | Intervention type | 68.6% | Food | 10 | SMD: 0.75 (95% CI: 0.52, 0.98) | <0.00001 | 234.35 | <0.00001 | 83% |
| | | | Supplement | 41 | SMD: 0.20 (95% CI: -0.36, 0.76) | 0.49 | 76.94 | <0.00001 | 88% |
| | Fiber type | 45.3% | Accepted prebiotic | 23 | SMD: 0.68 (95% CI: 0.38, 0.98) | <0.00001 | 117.8 | <0.00001 | 81% |
| | | | Candidate prebiotic | 13 | SMD: 0.77 (95% CI: 0.30, 1.24) | 0.001 | 86.19 | <0.00001 | 86% |
| | | | General fiber | 14 | SMD: 0.25 (95% CI: -0.16, 0.65) | 0.24 | 80.54 | <0.00001 | 84% |
| | | | | | | | | | |
| | Dose response | 8.8% | ≤5g/d | 11 | SMD: 0.51 (95% CI: 0.18, 0.84) | 0.003 | 33.52 | 0.0002 | 70% |
| | | | 5-10g/d | 18 | SMD: 0.48 (95% CI: 0.13, 0.84) | 0.007 | 133.22 | <0.00001 | 87% |
| | | | >10g/d | 22 | SMD: 0.85 (95% CI: 0.45, 1.25) | <0.00001 | 143.72 | <0.00001 | 85% |
| | | | | | | | | | |
| | | | | | | | | | |
| | Trial design | 77% | Cross-over | 30 | SMD: 0.44 (95% CI: 0.21, 0.66) | <0.00001 | 149.67 | <0.00001 | 81% |
| | | | Parallel | 21 | SMD: 0.98 (95% CI: 0.52, 1.44) | <0.00001 | 148.63 | <0.00001 | 87% |
| | Analysis method | 0% | Culture | 13 | SMD: 0.70 (95% CI: 0.07, 1.33) | 0.03 | 99.72 | <0.00001 | 88% |
| | | | qPCR | 11 | SMD: 0.62 (95% CI: 0.29, 0.94) | 0.0002 | 30.28 | 0.0008 | 67% |
| | | | FISH | 19 | SMD: 0.71 (95% CI: 0.31, 1.10) | 0.0004 | 187.79 | <0.00001 | 90% |
| | | | Sequencing | 4 | SMD: 0.61 (95% CI: 0.27, 0.95) | 0.0005 | 0.83 | 0.84 | 0% |
| | | | | | | | | | |
| <i>Lactobacillus</i> spp. | Intervention type | 0% | Food | 4 | SMD: 0.35 (95% CI: -0.46, 1.16) | 0.40 | 18.73 | 0.00003 | 84% |
| | | | Supplement | 19 | SMD: 0.16 (95% CI: 0.01, 0.31) | 0.04 | 19.27 | 0.38 | 7% |
| | Fiber type | 69.1% | Accepted prebiotic | 9 | SMD: 0.34 (95% CI: 0.13, 0.55) | 0.002 | 7.63 | 0.47 | 0% |
| | | | Candidate prebiotic | 7 | SMD: -0.06 (95% CI: -0.29, 0.16) | 0.58 | 3.52 | 0.74 | 0% |
| | | | General fiber | 7 | SMD: 0.22 (95% CI: -0.31, 0.75) | 0.42 | 23.23 | 0.0007 | 74% |
| | | | | | | | | | |
| | Dose | 0% | ≤5g/d | 6 | SMD: 0.16 (95% CI: -0.24, 0.56) | 0.44 | 9.67 | 0.09 | 48% |

| Outcome | Subgroup analysis | Subgroup difference (I ²) | Subgroups | Studies in subgroup (n) | Result | P | Heterogeneity | | |
|-------------------------------------|-------------------|---------------------------------------|------------|-------------------------|---|----------|------------------|--------|----------------|
| | | | | | Meta-analysis overall estimate (95% CI) | | Chi-squared test | P | I ² |
| <i>Faecalibacterium prausnitzii</i> | response | | 5-10g/d | 5 | SMD: 0.14 (95% CI: -0.12, 0.39) | 0.29 | 3.23 | 0.52 | 0% |
| | | | >10g/d | 12 | SMD: 0.29 (95% CI: -0.01, 0.59) | 0.06 | 26.08 | 0.006 | 58% |
| | | | Cross-over | 11 | SMD: 0.08 (95% CI: -0.09, 0.25) | 0.38 | 9.04 | 0.53 | 0% |
| | Trial design | 57.7% | Parallel | 12 | SMD: 0.37 (95% CI: 0.04, 0.70) | 0.03 | 26.8 | 0.005 | 59% |
| | | | Culture | 7 | SMD: 0.61 (95% CI: 0.13, 1.08) | 0.01 | 15.99 | 0.01 | 62% |
| | Analysis method | 55.1% | qPCR | 9 | SMD: 0.13 (95% CI: -0.07, 0.33) | 0.21 | 7.36 | 0.50 | 0% |
| | | | FISH | 2 | SMD: -0.15 (95% CI: -0.48, 0.18) | 0.37 | 0.01 | 0.94 | 0% |
| | | | Sequencing | 3 | SMD: 0.18 (95% CI: -0.19, 0.56) | 0.33 | 1.53 | 0.46 | 0% |
| | | | ≤5g/d | 3 | SMD: -0.10 (95% CI: -0.39, 0.19) | 0.51 | 2.71 | 0.26 | 26% |
| | Dose response | 38.0% | 5-10g/d | 6 | SMD: -0.05 (95% CI: -0.23, 0.13) | 0.57 | 2.55 | 0.77 | 0% |
| | | | >10g/d | 4 | SMD: 0.39 (95% CI: -0.09, 0.87) | 0.11 | 6.24 | 0.10 | 52% |
| | | | Cross-over | 8 | SMD: 0.06 (95% CI: -0.18, 0.29) | 0.63 | 12.71 | 0.08 | 45% |
| | Trial design | 53.6% | Parallel | 5 | SMD: 0.60 (95% CI: -0.09, 1.29) | 0.009 | 22.6 | 0.0002 | 82% |
| | | | Cross-over | 2 | SMD: -0.09 (95% CI: -0.46, 0.29) | 0.65 | 0.25 | 0.62 | 0% |
| <i>Roseburia</i> spp. | Trial design | 89.2% | Parallel | 2 | SMD: 0.71 (95% CI: 0.36, 1.06) | <0.00001 | 0.64 | 0.42 | 0% |

Supplemental Table 7: Outcomes of post hoc subgroup analyses undertaken

| Outcome | Subgroup analysis | Subgroup difference (I ²) | Subgroups | Studies in subgroup (n) | Result | Heterogeneity | | | |
|------------|-------------------|---------------------------------------|---------------------|-------------------------|---|---------------|------------------|----------|----------------|
| | | | | | Meta-analysis overall estimate (95% CI) | P | Chi-squared test | P | I ² |
| Total SCFA | Reporting method | 44.5% | Dry weight of feces | 6 | SMD: 0.02 (95% CI: -0.23, 0.26) | 0.89 | 2.81 | 0.73 | 0% |
| | | | Wet weight of feces | 6 | SMD: 0.25 (95% CI: 0.01, 0.49) | 0.04 | 0.80 | 0.98 | 0% |
| Acetate | Reporting method | 77.3% | Dry weight of feces | 6 | SMD: -0.08 (95% CI: -0.40, 0.25) | 0.65 | 10.26 | 0.07 | 51% |
| | | | Wet weight of feces | 10 | SMD: 0.69 (95% CI: 0.05, 1.33) | 0.03 | 98.97 | <0.00001 | 91% |
| Propionate | Reporting method | 0% | Dry weight of feces | 6 | SMD: -0.07 (95% CI: -0.33, 0.20) | 0.61 | 7.15 | 0.21 | 30% |
| | | | Wet weight of feces | 11 | SMD: 0.09 (95% CI: -0.26, 0.44) | 0.61 | 38.22 | <0.00001 | 74% |
| Butyrate | Reporting method | 74.1% | Dry weight of feces | 7 | SMD: 0.02 (95% CI: -0.18, 0.22) | 0.81 | 1.26 | 0.97 | 0% |
| | | | Wet weight of feces | 11 | SMD: 0.47 (95% CI: 0.07, 0.87) | 0.02 | 49.36 | <0.00001 | 80% |

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